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OM protein - protein search, using sw model

Run on: January 10, 2005, 19:28:46 ; Search time 40 Seconds
(without alignments)
951.663 Million cell updates/sec

Title: US-09-996-015-6

Perfect score: 3070

Sequence: 1 MWGLLLAALAFAPAVGALG.....GAKVPPDLRRRLRLRGQKD 574

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA.*
- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
 - 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
 - 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
 - 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
 - 5: /cgn2_6/ptodata/1/iaa/PCFUS_COMB.pep.*
 - 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2980	97.1	734	4	US-09-641-741-2
2	2976	96.9	734	3	US-08-706-216-2
3	2976	96.9	734	4	US-09-650-284B-2
4	2378.5	77.5	722	4	US-09-641-741-32
5	1398.5	45.6	764	4	US-09-641-741-31
6	1390.5	45.3	756	4	US-10-140-002-392
7	1180.5	38.5	1128	1	US-08-111-939-2
8	1180.5	38.5	1128	4	US-09-641-741-30
9	1180.5	38.5	1128	4	US-09-060-482-8
10	1166	38.0	845	4	US-09-641-741-29
11	1166	38.0	1158	4	US-09-060-482-2
12	1074	35.0	377	4	US-09-148-545-140
13	1071.5	34.9	719	4	US-09-641-741-28
14	1002.5	32.7	506	4	US-09-370-833-34
15	1002.5	32.7	506	4	US-09-854-133-34
16	815	26.5	208	4	US-09-148-545-207
17	758	24.7	484	1	US-08-111-939-12
18	616	20.1	458	3	US-09-233-989-9
19	609	19.8	438	1	US-08-111-939-17
20	609	19.8	641	3	US-09-233-989-10
21	582.5	19.0	454	3	US-09-233-989-4
22	576	18.8	476	3	US-09-233-989-3
23	574	18.7	476	3	US-09-233-989-2
24	574	18.7	476	4	US-09-917-254-67
25	572	18.6	476	3	US-09-233-989-6
26	565.5	18.4	435	1	US-08-111-939-14
27	564.5	18.4	435	1	US-08-111-939-16

28	564.5	18.4	435	1	US-08-452-262-2	Sequence 2, Appli
29	564.5	18.4	435	1	US-08-734-550-2	Sequence 2, Appli
30	564.5	18.4	435	5	PCT-US96-07528-2	Sequence 2, Appli
31	562.5	18.3	434	1	US-08-111-939-13	Sequence 13, Appli
32	562.5	18.3	434	3	US-09-233-989-7	Sequence 7, Appli
33	562.5	18.3	435	1	US-08-111-939-15	Sequence 15, Appli
34	487.5	15.9	561	3	US-09-233-989-5	Sequence 5, Appli
35	402.5	13.1	439	3	US-09-233-989-8	Sequence 8, Appli
36	402.5	13.1	443	4	US-09-976-594-527	Sequence 527, App
37	381.5	12.4	372	2	US-08-683-262B-64	Sequence 64, Appli
38	381.5	12.4	372	3	US-09-361-707-64	Sequence 64, Appli
39	282	9.2	109	1	US-08-111-939-19	Sequence 19, Appli
40	254	8.3	320	2	US-08-480-229C-20	Sequence 20, Appli
41	254	8.3	320	2	US-08-659-235C-20	Sequence 20, Appli
42	252.5	8.2	217	1	US-07-607-538C-3	Sequence 3, Appli
43	252.5	8.2	217	2	US-08-162-402B-3	Sequence 3, Appli
44	252.5	8.2	217	4	US-09-364-185-3	Sequence 3, Appli
45	252.5	8.2	218	1	US-07-607-538C-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-09-641-741-2

; Sequence 2, Application US/09641741

; Patent No. 6420155

; GENERAL INFORMATION:

; APPLICANT: Kerry E. Quinn

; APPLICANT: Curagen Corporation

; TITLE OF INVENTION: Aortic Carboxypeptidase-Like Proteins and Nucleic Acids

; TITLE OF INVENTION: encoding Same

; FILE REFERENCE: 15966-581

; CURRENT APPLICATION NUMBER: US/09/641,741

; CURRENT FILING DATE: 2000-08-18

; PRIOR APPLICATION NUMBER: 60/159,613

; PRIOR FILING DATE: 1999-10-14

; PRIOR APPLICATION NUMBER: 60/175,534

; PRIOR FILING DATE: 2000-01-12

; PRIOR APPLICATION NUMBER: 60/224,086

; PRIOR FILING DATE: 2000-08-09

; NUMBER OF SEQ ID NOS: 32

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2

; LENGTH: 734

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-641-741-2

Query Match 97.1%; Score 2980; DB 4; Length 734;

Best Local Similarity 78.2%; Pred.No 8.5e-277; Mismatches 0; Indels 160; Gaps 1;

Matches 574; Conservative 0

Qy	1	MWGLLLAALAFAPAVGALGAPNSVLGAPQCTTKVPGSTPALHSSPAQPPAETANGTS	60
Db	1	MWGLLLAALAFAPAVGALGAPNSVLGAPQCTTKVPGSTPALHSSPAQPPAETANGTS	60
Qy	61	EQHVRIRVKKKKVIMKKRKKLTTRPTPLVATGAVLTPPTAGTLPDAEKQETGCPPLGL	120
Db	61	EQHVRIRVKKKKVIMKKRKKLTTRPTPLVATGAVLTPPTAGTLPDAEKQETGCPPLGL	120
Qy	121	ESLRVSDSRLEASSSSOSFGLGPHRGRLNTQSGLEDGLYDGAWCAEBQDADPMFQVDAGH	180
Db	121	ESLRVSDSRLEASSSSOSFGLGPHRGRLNTQSGLEDGLYDGAWCAEBQDADPMFQVDAGH	180
Qy	181	PTFRSGVITQGRNSVWRVYDWTTSYKQFNSDRTWGRNSHSSGMDAVFPANSDPETPVL	240
Db	181	PTFRSGVITQGRNSVWRVYDWTTSYKQFNSDRTWGRNSHSSGMDAVFPANSDPETPVL	240
Qy	241	NLLPEQVQVAFIRLLPQTWLGQAPCLRAIBILACPVSDDNDLFLFAPAGSSSDPLDFQHH	300
Db	241	NLLPEQVQVAFIRLLPQTWLGQAPCLRAIBILACPVSDDNDLFLFAPAGSSSDPLDFQHH	300

; PRIOR FILING DATE: 1996-08-30
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 734
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-650-284B-2

Query Match 96.9%; Score 2976; DB 4; Length 734;
Best Local Similarity 78.1%; Pred. No. 2.1e-276;
Matches 573; Conservative 1; Mismatches 0; Indels 160; Gaps 1;

Qy 1 MWGLLLAALAPAVGAPALGAPRNSVLGLAQPGTKVPGSTPALHSSPAQPPAETANGTS 60
Db 1 MWGLLLAALAPAVGAPALGAPRNSVLGLAQPGTKVPGSTPALHSSPAQPPAETANGTS 60
Qy 61 EQHVRIRVIKKKVIKKRKKLTTRPTPLVTAGPLVTPPTAGTLDPAEQETGCPPLGL 120
Db 61 EQHVRIRVIKKKVIKKRKKLTTRPTPLVTAGPLVTPPTAGTLDPAEQETGCPPLGL 120
Qy 121 ESLRVSLSLEASSQSFGLGPHGRNLNIOGLEDGLYDGAMCAEQDADPWFQVDAGH 180
Db 121 ESLRVSLSLEASSQSFGLGPHGRNLNIOGLEDGLYDGAMCAEQDADPWFQVDAGH 180
Qy 181 PTFSGVITQGRNSVMRYDWTYSYKQVFSNDSRTWGSNRHSSGMDAVFPANSDPETPVL 240
Db 181 PTFSGVITQGRNSVMRYDWTYSYKQVFSNDSRTWGSNRHSSGMDAVFPANSDPETPVL 240
Qy 241 NLLPEQVAFIRLLPOTWLOGGAPCLRAEILACPVSDPNDLFLEAPASGSDPLDQHH 300
Db 241 NLLPEQVAFIRLLPOTWLOGGAPCLRAEILACPVSDPNDLFLEAPASGSDPLDQHH 300
Qy 301 NYKAMRKLKMQVQECNITRIYSIGKSYOGLKLYVMEMSDKPGHEHGEPEVRYVAGMH 360
Db 301 NYKAMRKLKMQVQECNITRIYSIGKSYOGLKLYVMEMSDKPGHEHGEPEVRYVAGMH 360
Qy 361 GNEALGRELLLLMQFLCHEFLRGNPRVTRLSEMR IHLLPSMNPDCGYEYAYHRGSELV 420
Db 361 GNEALGRELLLLMQFLCHEFLRGNPRVTRLSEMR IHLLPSMNPDCGYEYAYHRGSELV 420
Qy 421 WAEGRWNNQSIDLNHNFADLNTPLWEAQDDGKVPHI VPNHHLLPLPTTYTLPNATVAPETR 480
Db 421 WAEGRWNNQSIDLNHNFADLNTPLWEAQDDGKVPHI VPNHHLLPLPTTYTLPNATVAPETR 480
Qy 481 AVIKWMKRIPFVLSANLHGGLVVSYPFD----- 509
Db 481 AVIKWMKRIPFVLSANLHGGLVVSYPFD----- 509
Qy 510 ----- 509
Db 510 ----- 509
Qy 541 LAMQDTSRRPCHSQDFSVHGNINGADWHTVPGSMNDFSYLHTNCFEVTVLSCDKFPHE 600
Db 541 LAMQDTSRRPCHSQDFSVHGNINGADWHTVPGSMNDFSYLHTNCFEVTVLSCDKFPHE 600
Qy 510 ----- 509
Db 510 ----- 509
Qy 601 NELPQEWENNKDALLTYLEQVRMGIAGVVRDKOTELGIADAVIADGINHDVTTAWGGDY 660
Db 601 NELPQEWENNKDALLTYLEQVRMGIAGVVRDKOTELGIADAVIADGINHDVTTAWGGDY 660
Qy 510 -----VITASAEGYHSTVRCRVTPEEGPPCNFVLTKPKQRLRELLAAGAKVPP 560
Db 661 WRLLTGDIYVVTASAEGYHSTVRCRVTPEEGPPCNFVLTKPKQRLRELLAAGAKVPP 720
Qy 561 DLRRRLRLRGQKD 574
Db 721 DLRRRLRLRGQKD 734

RESULT 4
US-09-641-741-32
; Sequence 32, Application US/09641741
; Patent No. 6420155
; GENERAL INFORMATION:
; APPLICANT: Kerry E. Quinn
; APPLICANT: CuraGen Corporation

; TITLE OF INVENTION: Aortic Carboxypeptidase-Like Proteins and Nucleic Acids
; TITLE OF INVENTION: encoding Same
; FILE REFERENCE: 15966-581
; CURRENT APPLICATION NUMBER: US/09/641,741
; CURRENT FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: 60/159,613
; PRIOR FILING DATE: 1999-10-14
; PRIOR APPLICATION NUMBER: 60/175,534
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/224,086
; PRIOR FILING DATE: 2000-08-09
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32
; LENGTH: 722
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-641-741-32

Query Match 77.5%; Score 2378.5; DB 4; Length 722;
Best Local Similarity 64.3%; Pred. No. 4.4e-219;
Matches 471; Conservative 34; Mismatches 57; Indels 171; Gaps 5;

Qy 1 MWGLLLAALAPAVGAPALGAPRNSVLGLAQPGTKVPGSTPALHSSPAQPPAETANGTS 60
Db 1 MWGLLLAALAPAVGAPALGAPRNSVLGLAQPGTKVPGSTPALHSSPAQPPAETANGTS 60
Qy 61 EQHVRIRVIKKKVIKKRKKLTTRPTPLVTAGPLVTPPTAGTLDPAEQETGCPPLGL 120
Db 53 ERHVRIRVIKKKVIKKRKK--LRHPGLGTARPVVTHPAKTLTLPEKQEGCPCPLGL 110
Qy 121 ESLRVSLSLEASSQSFGLGPHGRNLNIOGLEDGLYDGAMCAEQDADPWFQVDAGH 180
Db 111 ESLRVSLSLEASSQSFGLGPHGRNLNIOGLEDGLYDGAMCAEQDADPWFQVDAGH 170
Qy 181 PTFSGVITQGRNSVMRYDWTYSYKQVFSNDSRTWGSNRHSSGMDAVFPANSDPETPVL 240
Db 171 PVRFAGIVTQGRNSVMRYDWTYSYKQVFSNDSRTWKSRLN-STGMDIVFPANSDAETPVL 229
Qy 241 NLLPEQVAFIRLLPOTWLOGGAPCLRAEILACPVSDPNDLFLEAPASGSDPLDQHH 300
Db 230 NLLPEQVAFIRLLPOTWLOGGAPCLRAEILACPVSDPNDLFLEAPASGSDPLDQHH 289
Qy 301 NYKAMRKLKMQVQECNITRIYSIGKSYOGLKLYVMEMSDKPGHEHGEPEVRYVAGMH 360
Db 290 NYKAMRKLKMQVQECNITRIYSIGKSHOGLKLYVMEMSDHGEHGEPEVRYVAGMH 349
Qy 361 GNEALGRELLLLMQFLCHEFLRGNPRVTRLSEMR IHLLPSMNPDCGYEYAYHRGSELV 420
Db 350 GNEALGRELLLLMQFLCHEFLRGNPRVTRLSEMR IHLLPSMNPDCGYEYAYHRGSELV 409
Qy 421 WAEGRWNNQSIDLNHNFADLNTPLWEAQDDGKVPHI VPNHHLLPLPTTYTLPNATVAPETR 480
Db 410 WAEGRWTHQSIDLNHNFADLNTOLWYAEADDGLVPDTPVNHLLPLPTTYTLPNATVAPETW 469
Qy 481 AVIKWMKRIPFVLSANLHGGLVVSYPFD----- 510
Db 470 AVIKWMKRIPFVLSANLHGGLVVSYPFD----- 529
Qy 511 ----- 510
Db 530 RAMQDTSRRPCHSQDFSLHGNVINGADWHTVPGSMNDFSYLHTNCFEVTVLSCDKFPHE 589
Qy 511 ----- 510
Db 590 KELPQEWENNKDALLTYLEQVRMGIAGVVRDKOTELGIADAVIADGINHDVTTAWGGDY 649
Qy 511 -----VITASAEGYHSTVRCRVTPEEGPPCNFVLTKPKQRLRELLAAGAKVPP 560
Db 650 WRLLTGDIYVVTASAEGYHSTVRCRVTPEEGPPCNFVLTKPKQRLRELLAAGAKVPP 709
Qy 561 DLRRRLRLRGQK 573

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Db      710  DLRRKLERLROK  722

RESULT 5
US-09-641-741-31
; Sequence 31, Application US/09641741
; Patent No. 6420155
; GENERAL INFORMATION:
; APPLICANT: Kery E. Quinn
; APPLICANT: Curagen Corporation
; TITLE OF INVENTION: Aortic Carboxypeptidase-Like Proteins and Nucleic Acids
; TITLE OF INVENTION: encoding same
; FILE REFERENCE: 45966-581
; CURRENT APPLICATION NUMBER: US/09/641,741
; CURRENT FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: 60/159,613
; PRIOR FILING DATE: 1999-10-14
; PRIOR APPLICATION NUMBER: 60/175,534
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/224,086
; PRIOR FILING DATE: 2000-08-09
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 31
; LENGTH: 764
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-641-741-31

Query Match
Best Local Similarity 45.6%; Score 1390.5; DB 4; Length 764;
Matches 301; Conservative 79; Mismatches 176; Indels 207; Gaps 0;

Qy      4  LLLAALAFAPAV-----GPAAGAP-----RNSVLGAQPGTKVPGSTPALH--- 4
Db      11  LALALVALAGVRAQGAFFEDPYGSOELWRGYYGHPEP-SPEPELFSFMSHEDL 6
Qy      46  ---SSPAQPAETANGTSEQHVIRVKKKVKIMKKRKLTLTRPTP----- 8
Db      70  RVEEQEQEHPQGHGTPK-----KAIPKKA--PKREKLVAETPPGKNSNRKGRSKN 1 2
Qy      90  LVTAGPLVTPPTAGTLDPAKQBTGCPPLGLESRLVSDSRLEASSQSFGLGPHGRGLNI 1 9
Db      123  LEKAASDDHGVPVAHEDVRE-----SCPLGLETLKITDFOLHASTSKRYGLGAHGRGLNI 1 8
Qy      150  QSGLEDGLYDGAWCAEQADPWFQDAGHPTRFSGVITQGRNSVMRYDWTYSYKVQFS 2 9
Db      179  QAGINENDFYDGAWCAGRNDLHGWIEVDARLTKFTGVITQGRNSLWLSDWYTSYKVMS 2 8
Qy      210  NDSRTWGRNSHSGMDVAPPANGSDPTVNLPLPEPQVAFIRLLPOTWLGQAGPCLRA 2 9
Db      239  NDSHTWTVKNGSG--DMIFEGNSEKEIPVLNLPVPMVARYIRINPQSFNDSGICRM 2 6
Qy      270  EILACVSDPNDLFLAPASGSDPLDFQHNHYKAMRKLKMKVQEQCPNITRIYSIGKSY 3 9
Db      297  EILGCPDPNNYHRRNEMTTDDLDKFHNHYKEMRQLMKVNMCPNITRIYNIKSH 3 6
Qy      330  QGLKLYMEMSDKPGHGLGEPEVRYVAGMHGNEALGRELLLLLOFLCHEFLRGNPVT 3 9
Db      357  QGLKLYAVISIDHPGHEVEPEFYIAGAHGNEVLGRELLLLHFLCQEYSAQNARIV 4 5
Qy      390  RLLSEMRHLLPSMNPDPGEIAYHRGSELVGAEGRWNNQSIDLNHNFTADLTPLWEAQD 4 3
Db      417  RLVEETRIHLPSLNDPDGEKAYEGGSELGWSLGRWTHDGDINNPFDPNLSLWEAED 4 5
Qy      450  DGKVPHIVNHLPLPTYYTLNATVAPETRAVIAKMKRIPVLSANLHGGSELVVSYPFD 5 3
Db      477  QONAPRKVPNHXIAIPEWFLSENAIVATETRAVIAMKXIPVLSGGLQGGSELVVAYPD 5 5
Qy      510  M----- 5 3
Db      537  MVRSLMKTOEHTPTPDHVRWLAYSASTHRLMTDARRRVCHTDFQKEGSTVNGASWH 5 5

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Qy      511  ----- 510
Db      597  TVAGSLNDFSYLHTNCFELSIYVGCDCYPHESELPEEWNNRESLIVFMEQVHRGIGKIV 656
Qy      511  -----VTASAEYSHSVTRNCRVTPE 530
Db      657  RLOQKGISNAVISVEGVNHDIRTASDGDYWRLLNPGYVVTAKAEGFITKNCMVGVD 716
Qy      531  EGFPFCNFVLTPTKQKORRELAAGAAGKVPDPDLRRRLRLRLOK 573
Db      717  MGATRCDFTLTKTNLARIEMETFGQFVSLPSRLRLGRK 759

RESULT 6
US-10-140-002-392
; Sequence 392, Application US/10140002
; Patent No. 6725730
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: ACIDS ENCODING THE SAME
; CURRENT APPLICATION NUMBER: US/10/140,002
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 392
; LENGTH: 756
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-140-002-392

Query Match
Best Local Similarity 45.3%; Score 1390.5; DB 4; Length 756;
Matches 299; Conservative 76; Mismatches 185; Indels 187; Gaps 8;

Qy      4  LLLAALAFAPAVGPAAGAP-----RNSVLGAQPGTKVPGSTPALHSSPAQSPAE 54
Db      15  LLAVTLAGVGAQGAALDDPDYGOEISWRBPPYARPEP---ELETFSPPL---PAGSGEE 68
Qy      55  TANGTSEQHVIRVIRVKKKVKIMKKRKLTLTRPTPLVTAGPLVTPPT---PAGTLDPAA-- 108
Db      69  WERRPOEPRPKPKATPKKA--PKREKSAPEPPPGKHKNKVMRTKSKSEKANDHSHVR 126
Qy      109  ---EKQBTGCPPLGLESRLVSDSRLEASSQSFGLGPHGRGLNIQSGLEDGLYDGAWCA 165
Db      127  VAREDVRESCPPLGLETLKITDFOLHASTVKRYGLGAHGRGLNIQAGINENDFYDGAWCA 186
Qy      166  EQQADPWFQDAGHPTRFSGVITQGRNSVMRYDWTYSYKVQFSNDSRTWGRNSHSGM 225
Db      187  GRNDLQWIEVDARLRTFTGVITQGRNSLWLSDWYTSYKVMSNDSHTWTVKNGSG-- 244
Qy      226  DAVFPANGSDPTVNLPLPEPQVAFIRLLPOTWLGQAGPCLRAEILACVSDPNDLFL 285
Db      245  DMIFEGNSEKEIPVLNLPVPMVARYIRINPQSFNDSGICMRMELGCPDPNPNYHRR 304
Qy      286  APASGSDPLDFQHNHYKAMRKLKMKVQEQCPNITRIYSIGKSYQGLKLYMEMSDKPG 345

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; PRIOR FILING DATE: 2000-01-12
 ; PRIOR APPLICATION NUMBER: 60/224,086
 ; EARLIER FILING DATE: 2000-08-09
 ; NUMBER OF SEQ ID NOS: 32
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 10
 ; LENGTH: 1128
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-09-641-741-30

Query Match 38.5%; Score 1180.5; DB 4; Length 1128;
 Best Local Similarity 37.8%; Pred. No. 8.5e-104;
 Matches 246; Conservative 75; Mismatches 134; Indels 195; Gaps 6;
 QY 107 PAEKQETGCPPLGLESRLVSDSRLAASSOSFGLGPHRGLNLTQSGLEQDGLYDGAACAE 1 6
 DB 370 PVEKIK--CPPIGMESHRIEDNQIRASSMLRHGLGAQGRGLNMQAGANEDDDYDGAACAE 4 7
 QY 167 EQADAPFQVDAGHPTRFSGVITQGRNSVMRYDWVTSYKQVFSNDSRTWMSRHHSSGMD 2 6
 DB 428 DESQTMIEVDTRTRFTGTGTQGRDSSIHDDFVTTFVGFNSDQTVMWYTNGYEEM- 4 6
 QY 227 AVFPANSDPTPVNLNLLPEPOVARFIRLLPOTLQGGAPCLRAEILACPVSDPNDLFLEA 2 6
 DB 487 -TFYGNVBDKTPVLSLPEPVVAFRIYPLTW--NGSLCMRLEVLCGCVTPVYSYQAQ 5 3
 QY 287 PASGSSDPLDFQHHNYKAMRKLKQVQOCNITRIYSIGKSYQGLKLYVMEMSDKPGEH 3 6
 DB 544 EVV-TTDSLDPRHHSYKDMRQMKAVNEECPTITRTYSLGKSRGLKIYAMEISDNPGDH 6 2
 QY 347 ELGEPEVRYVAGHNGEALGRELLELLLMQFLCHEFLRGNPRVTRLLSEMRTHLLPSMNP 4 6
 DB 603 ELGEPEFRYTAGIHGNEVLGRELLELLLMQVLCQYRDGNPRVRLVQDTRIHLVPSLND 6 2
 QY 407 GYELAHRGSELVAGWAGRWNNQSIDLNHNFAADLNTPLWEAODDGKVPPIVPHNHLPLPT 4 6
 DB 663 GYEVAAQMGSEFGNVALGLWTEGDFIDFDPDLNSVLAAEKKWVPYRVNNNLPPE 7 2
 QY 467 YITLPNATVAPETRAVTKMKRIPFVLSANLHGGELVVSYPFDM----- 5 0
 DB 723 RYLSPDATVSTEVRAIIISWMEKNPFVLGANGGERLVSPYDMARTPSQEOALLAEALAA 7 2
 QY 511 ----- 5 0
 DB 783 ARGEDDDGVSEAQETPDHAIFRWLAISFASAHLTMTPEYRGCGQAQDYTSGMGIVNGAKW 8 2
 QY 511 ----- 5 0
 DB 843 NPSRGTNDFSYLHTNCLSVLGCDFPHESELPREWENKKEALLTFMEQVHRIGKV 9 2
 QY 511 ----- 5 0
 DB 903 VTDEQGIPIANATISVSGINHGKVTASGGDYWRILNPGEYRVTAHAEGYTSSAKICNDY 9 2
 QY 530 EGGPPFCNFVLTKPKORRELLAAGAKVP-----PDLRRRLER 568
 DB 963 DIGATOCNFILARSNWKRIREILAMNGNRPILGVDPSPRMTPOQRMMQOR 1012

RESULT 9
 US-09-060-482-8
 ; Sequence 8, Application US/09060482
 ; Patent No. 6468766
 ; GENERAL INFORMATION:
 ; APPLICANT: Lee, Mu-En
 ; APPLICANT: Layne, Matthew D.
 ; APPLICANT: Yet, Shaw-Fang
 ; TITLE OF INVENTION: AORTIC CARDOXYPEPTIDASE-LIKE POLYPEPTIDE
 ; FILE REFERENCE: 05433/036001
 ; CURRENT APPLICATION NUMBER: US/09/060,482
 ; CURRENT FILING DATE: 1998-04-15
 ; PRIOR APPLICATION NUMBER: US 06/818,009

; EARLIER FILING DATE: 1997-03-14
 ; EARLIER APPLICATION NUMBER: US 60/013,439
 ; EARLIER FILING DATE: 1996-03-15
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 8
 ; LENGTH: 1128
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-09-060-482-8

Query Match 38.5%; Score 1180.5; DB 4; Length 1128;
 Best Local Similarity 37.8%; Pred. No. 8.5e-104;
 Matches 246; Conservative 75; Mismatches 134; Indels 195; Gaps 6;
 QY 107 PAEKQETGCPPLGLESRLVSDSRLAASSOSFGLGPHRGLNLTQSGLEQDGLYDGAACAE 166
 DB 370 PVEKIK--CPPIGMESHRIEDNQIRASSMLRHGLGAQGRGLNMQAGANEDDDYDGAACAE 427
 QY 167 EQADAPFQVDAGHPTRFSGVITQGRNSVMRYDWVTSYKQVFSNDSRTWMSRHHSSGMD 226
 DB 428 DESQTMIEVDTRTRFTGTGTQGRDSSIHDDFVTTFVGFNSDQTVMWYTNGYEEM- 486
 QY 227 AVFPANSDPTPVNLNLLPEPOVARFIRLLPOTLQGGAPCLRAEILACPVSDPNDLFLEA 286
 DB 487 -TFYGNVBDKTPVLSLPEPVVAFRIYPLTW--NGSLCMRLEVLCGCVTPVYSYQAQ 543
 QY 287 PASGSSDPLDFQHHNYKAMRKLKQVQOCNITRIYSIGKSYQGLKLYVMEMSDKPGEH 346
 DB 544 EVV-TTDSLDPRHHSYKDMRQMKAVNEECPTITRTYSLGKSRGLKIYAMEISDNPGDH 602
 QY 347 ELGEPEVRYVAGHNGEALGRELLELLLMQFLCHEFLRGNPRVTRLLSEMRTHLLPSMNP 406
 DB 603 ELGEPEFRYTAGIHGNEVLGRELLELLLMQVLCQYRDGNPRVRLVQDTRIHLVPSLND 662
 QY 407 GYELAHRGSELVAGWAGRWNNQSIDLNHNFAADLNTPLWEAODDGKVPPIVPHNHLPLPT 466
 DB 663 GYEVAAQMGSEFGNVALGLWTEGDFIDFDPDLNSVLAAEKKWVPYRVNNNLPPE 722
 QY 467 YITLPNATVAPETRAVTKMKRIPFVLSANLHGGELVVSYPFDM----- 510
 DB 723 RYLSPDATVSTEVRAIIISWMEKNPFVLGANGGERLVSPYDMARTPSQEOALLAEALAA 782
 QY 511 ----- 510
 DB 783 ARGEDDDGVSEAQETPDHAIFRWLAISFASAHLTMTPEYRGCGQAQDYTSGMGIVNGAKW 842
 QY 511 ----- 510
 DB 843 NPSRGTNDFSYLHTNCLSVLGCDFPHESELPREWENKKEALLTFMEQVHRIGKV 902
 QY 511 ----- 510
 DB 903 VTDEQGIPIANATISVSGINHGKVTASGGDYWRILNPGEYRVTAHAEGYTSSAKICNDY 962
 QY 530 EGGPPFCNFVLTKPKORRELLAAGAKVP-----PDLRRRLER 568
 DB 963 DIGATOCNFILARSNWKRIREILAMNGNRPILGVDPSPRMTPOQRMMQOR 1012

RESULT 10
 US-09-641-741-29
 ; Sequence 29, Application US/09641741
 ; Patent No. 6420155
 ; GENERAL INFORMATION:
 ; APPLICANT: Kerry E. Quinn
 ; APPLICANT: Curagen Corporation
 ; TITLE OF INVENTION: Aortic Carboxypeptidase-Like Proteins and Nucleic Acids
 ; FILE REFERENCE: 15966-581
 ; CURRENT APPLICATION NUMBER: US/09/641,741
 ; CURRENT FILING DATE: 2000-08-18
 ; PRIOR APPLICATION NUMBER: 60/159,613

; PRIOR FILING DATE: 1999-10-14
; PRIOR APPLICATION NUMBER: 60/175,534
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/224,086
; PRIOR FILING DATE: 2000-08-09
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 29
; TYPE: PRT
; LENGTH: 845
; ORGANISM: Homo sapiens
US-09-641-741-29

Query Match 38.0%; Score 1166; DB 4; Length 845;
Best Local Similarity 37.7%; Pred. No. 1.3e-102;
Matches 249; Conservative 74; Mismatches 136; Indels 202; Gaps 8;

QY 107 PAEKQETGCPPLGLESIRVSDSRLEASSQSFGLPGRRLNLTOSGLEDDGLYDGAACAE 166
DB 66 PTEKVK--CPPIGMESHRIEDNQIRASSMLRHGLGAQRRLNMQTGATEDDDYDGAACAE 123
QY 167 EQADAPMFQVDAGHPTFRFSGVITQGRNSVMRYDWVTISKYQVFNDSRTWGSRNHSSGMD 226
DB 124 DDARTQWIEVDTRTRFTGVIITQGRDSSIHDDFVITFFVGFNSDSTQWMTYNGYEEM- 182
QY 227 AVFPANSDPTPVNLNLPPEQVAFIRLLPQTLQGGAPCLRAEILACPVSDPNDLFLFA 286
DB 183 -TFHGNVDKDTPLSELPEPVAFIRIYPLTW--NGSLCWLLEVLGCSVAPVYSYAQN 239
QY 287 PASGSDPLDFQHHNYKAMKLMKQVQECNPTIRIYSIGKSYOGLKLYWMSDKRGEH 346
DB 240 EVV-ATDLDLFRHSHYKDMRQMLKVNNECPTITRTYSLGKSRGLKIYAMEISDNPEH 298
QY 347 ELGEPEVRYVAGHMGNEALGRELILLMQFLCHEFLRGNPRVTRLISEMIRHLLPSMNP 406
DB 299 ELGEPEFRYTAGIHGNEVLGRELILLMQFLCHEFLRGNPRVTRLISEMIRHLLPSMNP 358
QY 407 GYBIAHRGSELVGMABGRWNNSIDLNHNFADLNTPLWBAQDDGKVPHTVPNNHLLPLPT 466
DB 359 GYEVAQMGSFEGNWALGLWTEBGFDFEDFPLNSVLWGAEERKWPYRVPNNLPIPE 418
QY 467 YYTLPNATVAPETRAVIKWKRIPTFVLSANLHGSELVVSYPFDM----- 510
DB 419 RYLSPDATVSTEVRAITAMNEKNPFVLGANLNGERLVSYPDMARTPTQOQLLAAMAA 478
QY 511 ----- 510
DB 479 ARGEDEVESEAQETPDHAIFRWLAISFASAHLLTLEPYRGCGQAQDYTGGMGIVNGAKW 538
QY 511 ----- 510
DB 539 NPRTGTINDFSYLHTNCLLSFYLGCDKFPHESELPREWENKEALLTFMEQVHRGKGV 598
QY 511 ----- 510
DB 599 VTDEQGIPIANATISVGINHGKVTASGGDYWRILNPGEYRVTAHAEGYTPSAKTCNV 658
QY 530 EGGPFCNFVLTKTPKORLELLAAGAKVP-----PDLR-----RLRG 571
DB 659 DIGATQCNFILARSNNKRIREIMAMNGNRPIPHIDPSRPMTPPOORLQORRLQRLRA 718
QY 572 Q 572
DB 719 Q 719

RESULT 11
US-09-060-482-2
; Sequence 2, Application US/09060482
; Patent No. 6468766
; GENERAL INFORMATION:
; APPLICANT: Lee, Mu-En
; APPLICANT: Layne, Matthew D.

; APPLICANT: Yet, Shaw-Fang
; TITLE OF INVENTION: AORTIC CARDOXYPEPTIDASE-LIKE POLYPEPTIDE
; FILE REFERENCE: 05433/036001
; CURRENT APPLICATION NUMBER: US/09/060,482
; CURRENT FILING DATE: 1998-04-15
; EARLIER APPLICATION NUMBER: US 081818,009
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: US 601013,439
; EARLIER FILING DATE: 1996-03-15
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 1158
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-060-482-2

Query Match 38.0%; Score 1166; DB 4; Length 1158;
Best Local Similarity 37.7%; Pred. No. 2.2e-102;
Matches 249; Conservative 74; Mismatches 136; Indels 202; Gaps 8;

QY 107 PAEKQETGCPPLGLESIRVSDSRLEASSQSFGLPGRRLNLTOSGLEDDGLYDGAACAE 166
DB 379 PTEKVK--CPPIGMESHRIEDNQIRASSMLRHGLGAQRRLNMQTGATEDDDYDGAACAE 436
QY 167 EQADAPMFQVDAGHPTFRFSGVITQGRNSVMRYDWVTISKYQVFNDSRTWGSRNHSSGMD 226
DB 437 DDARTQWIEVDTRTRFTGVIITQGRDSSIHDDFVITFFVGFNSDSTQWMTYNGYEEM- 495
QY 227 AVFPANSDPTPVNLNLPPEQVAFIRLLPQTLQGGAPCLRAEILACPVSDPNDLFLFA 286
DB 496 -TFHGNVDKDTPLSELPEPVAFIRIYPLTW--NGSLCWLLEVLGCSVAPVYSYAQN 552
QY 287 PASGSDPLDFQHHNYKAMKLMKQVQECNPTIRIYSIGKSYOGLKLYWMSDKRGEH 346
DB 553 EVV-ATDLDLFRHSHYKDMRQMLKVNNECPTITRTYSLGKSRGLKIYAMEISDNPEH 611
QY 347 ELGEPEVRYVAGHMGNEALGRELILLMQFLCHEFLRGNPRVTRLISEMIRHLLPSMNP 406
DB 612 ELGEPEFRYTAGIHGNEVLGRELILLMQFLCHEFLRGNPRVTRLISEMIRHLLPSMNP 671
QY 407 GYBIAHRGSELVGMABGRWNNSIDLNHNFADLNTPLWBAQDDGKVPHTVPNNHLLPLPT 466
DB 672 GYEVAQMGSFEGNWALGLWTEBGFDFEDFPLNSVLWGAEERKWPYRVPNNLPIPE 731
QY 467 YYTLPNATVAPETRAVIKWKRIPTFVLSANLHGSELVVSYPFDM----- 510
DB 732 RYLSPDATVSTEVRAITAMNEKNPFVLGANLNGERLVSYPDMARTPTQOQLLAAMAA 791
QY 511 ----- 510
DB 792 ARGEDEVESEAQETPDHAIFRWLAISFASAHLLTLEPYRGCGQAQDYTGGMGIVNGAKW 851
QY 511 ----- 510
DB 852 NPRTGTINDFSYLHTNCLLSFYLGCDKFPHESELPREWENKEALLTFMEQVHRGKGV 911
QY 511 ----- 510
DB 912 VTDEQGIPIANATISVGINHGKVTASGGDYWRILNPGEYRVTAHAEGYTPSAKTCNV 971
QY 530 EGGPFCNFVLTKTPKORLELLAAGAKVP-----PDLR-----PDLR-----RLRG 571
DB 972 DIGATQCNFILARSNNKRIREIMAMNGNRPIPHIDPSRPMTPPOORLQORRLQRLRA 1031
QY 572 Q 572
DB 1032 Q 1032

RESULT 12
US-09-148-545-140
; Sequence 140, Application US/09148545

Patent No. 6590075
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 70 Human Secreted Proteins
FILE REFERENCE: P2001P1
CURRENT APPLICATION NUMBER: US/09/148,545
CURRENT FILING DATE: 1998-09-04
EARLIER APPLICATION NUMBER: PCT/US98/04482
EARLIER FILING DATE: 1998-03-06
EARLIER APPLICATION NUMBER: 60/040,162
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,333
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/038,621
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,161
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,626
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,334
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,336
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,163
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/047,615
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,600
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,597
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,502
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EARLIER APPLICATION NUMBER: 60/047,633
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,583
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,617
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,618
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,503
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,592
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,581
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,584
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,500
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,587
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,492
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EARLIER APPLICATION NUMBER: 60/047,613
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,582
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,596
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,612
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,632
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EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,580
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,568
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,314
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,569
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,311
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,671
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EARLIER APPLICATION NUMBER: 60/043,672
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,315
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/048,974
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/056,886
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,877
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,889
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,893
EARLIER FILING DATE: 1997-08-22
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EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,878
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,662
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,872
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,882
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,637
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,903
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,888
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,879
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,880
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,894
EARLIER FILING DATE: 1997-08-22
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EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,636
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,874
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,910
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,864
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,631
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,845
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,892
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/047,595
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/057,761
EARLIER FILING DATE: 05-Sep-1997
EARLIER APPLICATION NUMBER: 60/047,599

QY	510	-----	509
Db	241	HENELPQEWENNKDALLTYLEQVRMGIAGVVRDKDTELGADAVIAVDGINHDTVTTMGG	300
QY	510	-----MVTASAGYHSVTRNCRVTPEEGPPCNFVLTTKTKPQRLRELLAAGAKV	558
Db	301	DYWRLLTPGDYVMVTASAGYHSVTRNCRVTPEEGPPCNFVLTTKTKPQRLRELLAAGAKV	360
QY	559	PPDLRRRLRLRGQKD 574	
Db	361	PPDLRRRLRLRGQKD 376	
RESULT 13			
US-09-641-741-28			
; Sequence 28, Application US/09641741			
; Patent No. 6420155			
; GENERAL INFORMATION:			
; APPLICANT: Kerry E. Quinn			
; APPLICANT: Curagen Corporation			
; TITLE OF INVENTION: Aortic Carboxypeptidase-Like Proteins and Nucleic Acids			
; TITLE OF INVENTION: encoding Same			
; FILE REFERENCE: 15966-581			
; CURRENT APPLICATION NUMBER: US/09/641,741			
; CURRENT FILING DATE: 2000-08-18			
; PRIOR APPLICATION NUMBER: 60/159,613			
; PRIOR FILING DATE: 1999-10-14			
; PRIOR APPLICATION NUMBER: 60/175,534			
; PRIOR FILING DATE: 2000-01-12			
; PRIOR APPLICATION NUMBER: 60/224,086			
; PRIOR FILING DATE: 2000-08-09			
; NUMBER OF SEQ ID NOS: 32			
; SOFTWARE: PatentIn Ver. 2.0			
; SEQ ID NO 28			
; LENGTH: 719			
; TYPE: PRT			
; ORGANISM: Mus musculus			
US-09-641-741-28			
Query Match 34.9%; Score 1071.5; DB 4; Length 719;			
Best Local Similarity 36.8%; Pred. No. 1.2e-93;			
Matches 224; Conservative 68; Mismatches 123; Indels 193; Gaps 5			
QY	149	IQSGLEDGLYDGAWCABEQADPMFQVDAGHPTFRFSGVITQGRNSVMRYDWTISYKVF	208
Db	1	MQAGANEDDYDGAWCABEDESQTQWIEVDTRRTFTGVTITQGRDSSIHDDFVTFVGF	60
QY	209	SNDSRTWGSNRHSSGMDAVFPANSDPETVNLNLPPEQVAFIRLLPQTLLQGGAPCLR	268
Db	61	SNDSQTVMVMTNGYEEM--TFYGNVDKDTPLVSELPEPVARFIRIYPLTW--NGSLCMR	116
QY	269	ABILACPVSDPNDLFLFAPASGSDPLDFQHNHYKAMRKLKMKQVQEQCPNTRIYSICKS	328
Db	117	LEVLCGPTVPVYSYAQNEV--TTDSLDFRHHSYKDMRQLMKAVNEECPTTIRTSYLGKS	175
QY	329	YQGLKLYWEMSDKGEHELGEPEVRYVAGMGNELGRELLLLMQFLCHEFLRGNPRV	388
Db	176	SRGLKIYAMEISDNFGDHELGEPEPYTAGIHGNEVLGRELLLLMQVLCQEYRDGNPRV	235
QY	389	TRLLSEMRTHLLPSMNPDCYEIAYHRGSELVGAEGRWNNQSIDLNHNFADLNTPLMBAQ	448
Db	236	RNLVQDTRTHLVPSLNPDCYEVAQMGSEFGNWLGLWTEEGFDIFEDFPDLNSVLMAAE	295
QY	449	DGKQPHIVPNHLLPLPTTYTLPNATVAPETRAVIKWKRIPFVLNHLGSELVVSYPF	508
Db	296	EKKWVPYRPNNNLPIPERYLSPDATVSTEVRAIISWMKPNFVLGALNGERLVSYPY	355
QY	509	DM-----	510
Db	356	DWARTPSQQLLAELAAARGEDDDGCVSEAQETPDHAIFRWLAIISFASAHUTMTPEYRG	415
QY	511	-----	510

Db 416 CQAQDYTSGMGIUNGAKNPRSGTENDFSYLHTNCLLSVYLGCDKPPHSELPREWENN 4 15
QY 511 -----Y : 1
Db 476 KEALLTFMEQVHRGIGVTVDEGCIPIANATISVGINHGVKTASGQDYWRILNPGYERV : 15
QY 512 TASAEGYHSVTRNCRVTFEBGPPCPNFVLTKPKQRLRELLAAGAKVP -----P : 10
Db 536 TAAAGYTSAKICNDYDIDGATQCNCNFILARSWNKRIREILAMNGNRPILRVDPPSRPMTF : 15
QY 561 DLRRLER 568
Db 596 QRRMQOR 603
RESULT 14
US-09-370-838-34
; Sequence 34, Application US/09370838
; Patent No. 644425
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Mohamath, Raodoh
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF
; - TITLE OF INVENTION: LUNG CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.475C1
; CURRENT APPLICATION NUMBER: US/09/370,838
; CURRENT FILING DATE: 1999-08-05
; EARLIER FILING DATE: 1999-04-02
; NUMBER OF SEQ ID NOS: 289
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 34
; LENGTH: 506
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-370-838-34
Query Match 32.7%; Score 1002.5; DB 4; Length 506;
Best Local Similarity 39.9%; Pred. No. 2.9e-87;
Matches 200; Conservative 51; Mismatches 91; Indels 159; Gaps 1;
QY 232 NSDPETPVNLLPEPOVARFIRLLPOTWLOQCAPCLRAEILACPVSDPNDLFLEAPASGS 2 1
Db 1 NSEKEIPVNLPEPVMVARYIRINPQSWFDNGSICMRMEILGCLPLDPNNYHRRNEMTT 6
QY 292 SDPLDFQHHNYKAMRKLKMQVQEQCPNITRIYSIGKSYQGLKLYVMEMSDKPGHEHGE 3 1
Db 61 TDOLDPFGHHNYKEMRQMKVVMEMCPNITRIYNGKSHQGLKLYAVEISDHPGHEVEGEP 1 0
QY 352 EYRVVAGMHGNEALGRELLLLMQFLCHFEFLRGNPRVTRLSEMRHLLPSMNPDPGYEIA 4 1
Db 121 EFHYIAGAHGNEVLGRELLLLHFLCQEYSAQNARIIVRLVEETRIHILPSLNPDPGYEKA 1 0
QY 412 YHRGSELVWAGRWNNQSIDLNHNPADLNTPLWEAQDDGKVPVHVPNNHLLPLPTYTLP 4 1
Db 181 YEGGSELGWSLGRWTHDIDINNPFPLNSLLWEAEDQQNAPRKVPNNHYIAIPEWFLSE 2 0
QY 472 NATVAPETRAVTKWKRIPFVLSANLHGSELVVSYPFDM----- 5 0
Db 241 NATVATETRAVIAMWEKIPFVLGGLQGGELVVAIPYDMVRSWLKWTQEHPTPTDDHVPFW 3 0
QY 511 ----- 5 0
Db 301 LAYSASTHRLMTDARRRVCHTEDFKKEGTVNGASWHTVAGSLNDFSYLHTNCFELSIY 3 0
QY 511 ----- 5 0
Db 361 VQCDKYPHESELPEWENNRESLIVFMEQVHRGIGIVRDLQGGKISNAVISVEGVNNDI 4 0
QY 511 -----VTASAEGYHSVTRNCRVTFEBGPPCPNFVLTKPKQRLRELL 5 2

Db 421 RTASDGDYWRLLNPGEYVVTAKAEGFITSTKNCMVGYDMGATRCDFTLTKTNLARIREIM 480
QY 553 AAGAKVPPDLRRRLERLRGQK 573
Db 481 ETFGKQVPSLPSRRLKLRGRK 501
RESULT 15
US-09-854-133-34
; Sequence 34, Application US/09854133
; Patent No. 6759508
; GENERAL INFORMATION:
; APPLICANT: Lodes, Michael J.
; APPLICANT: Mohamath, Raodoh
; APPLICANT: Henderson, Robert A.
; APPLICANT: Benson, Darin R.
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; - TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.475C10
; CURRENT APPLICATION NUMBER: US/09/854,133
; CURRENT FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 735
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 34
; LENGTH: 506
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-854-133-34
Query Match 32.7%; Score 1002.5; DB 4; Length 506;
Best Local Similarity 39.9%; Pred. No. 2.9e-87;
Matches 200; Conservative 51; Mismatches 91; Indels 159; Gaps 1;
QY 232 NSDPETPVNLLPEPOVARFIRLLPOTWLOQCAPCLRAEILACPVSDPNDLFLEAPASGS 291
Db 1 NSEKEIPVNLPEPVMVARYIRINPQSWFDNGSICMRMEILGCLPLDPNNYHRRNEMTT 60
QY 292 SDPLDFQHHNYKAMRKLKMQVQEQCPNITRIYSIGKSYQGLKLYVMEMSDKPGHEHGE 351
Db 61 TDOLDPFGHHNYKEMRQMKVVMEMCPNITRIYNGKSHQGLKLYAVEISDHPGHEVEGEP 120
QY 352 EYRVVAGMHGNEALGRELLLLMQFLCHFEFLRGNPRVTRLSEMRHLLPSMNPDPGYEIA 411
Db 121 EFHYIAGAHGNEVLGRELLLLHFLCQEYSAQNARIIVRLVEETRIHILPSLNPDPGYEKA 180
QY 412 YHRGSELVWAGRWNNQSIDLNHNPADLNTPLWEAQDDGKVPVHVPNNHLLPLPTYTLP 471
Db 181 YEGGSELGWSLGRWTHDIDINNPFPLNSLLWEAEDQQNAPRKVPNNHYIAIPEWFLSE 240
QY 472 NATVAPETRAVTKWKRIPFVLSANLHGSELVVSYPFDM----- 510
Db 241 NATVATETRAVIAMWEKIPFVLGGLQGGELVVAIPYDMVRSWLKWTQEHPTPTDDHVPFW 300
QY 511 ----- 510
Db 301 LAYSASTHRLMTDARRRVCHTEDFKKEGTVNGASWHTVAGSLNDFSYLHTNCFELSIY 360
QY 511 ----- 510
Db 361 VQCDKYPHESELPEWENNRESLIVFMEQVHRGIGIVRDLQGGKISNAVISVEGVNNDI 420
QY 511 -----VTASAEGYHSVTRNCRVTFEBGPPCPNFVLTKPKQRLRELL 552
Db 421 RTASDGDYWRLLNPGEYVVTAKAEGFITSTKNCMVGYDMGATRCDFTLTKTNLARIREIM 480
QY 553 AAGAKVPPDLRRRLERLRGQK 573
Db 481 ETFGKQVPSLPSRRLKLRGRK 501

Search completed: January 10, 2005, 19:39:06

Job time : 54 secs

· his Page Blank (uspto)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 10, 2005, 19:19:34 ; Search time 154 Seconds
(without alignments)

1337.082 Million cell updates/sec

Title: US-09-996-015-6

Perfect score: 3070

Sequence: 1 MWGLLALAAFAPAVAGPALG.....GAKVPPDLRRRLRLRGQKD 574

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3070	100.0	574	7 ADC71542	Adc71542 Human NOV
2	3070	100.0	574	8 ADN33953	Adn33953 Human NOV
3	3070	100.0	574	8 ADO42303	Ado42303 Human NOV
4	2980	97.1	734	4 AAB47184	Aab47184 ACPLX pro
5	2980	97.1	734	4 AAG65917	Aag65917 Amino aci
6	2980	97.1	734	7 ADC71546	Adc71546 Human NOV
7	2980	97.1	734	7 ADP65320	Adp65320 Human met
8	2980	97.1	734	8 ADN33957	Adn33957 Human nov
9	2980	97.1	734	8 ADO42301	Ado42301 Human NOV
10	2980	97.1	734	8 ADO42305	Ado42305 Human NOV
11	2980	97.1	734	8 ADO42307	Ado42307 Human NOV
12	2976	96.9	734	4 AAB36174	Aab36174 Human APG
13	2976	96.9	734	7 ADJ63969	Adj63969 Human APG
14	2976	96.9	734	4 AAU29252	Aau29252 Human PRO
15	2975	96.9	734	6 ABUS8628	Abu8628 Human PRO
16	2975	96.9	734	6 ABUS8628	Abu8628 Human PRO
17	2975	96.9	734	6 ABUS8628	Abu8628 Human PRO
18	2975	96.9	734	6 ABUS8628	Abu8628 Human PRO
19	2975	96.9	734	6 ABUS8628	Abu8628 Human PRO
20	2975	96.9	734	6 ABUS8628	Abu8628 Human PRO
21	2975	96.9	734	6 ABUS8628	Abu8628 Human PRO
22	2975	96.9	734	6 ABUS8628	Abu8628 Human PRO
23	2975	96.9	734	6 ABUS8628	Abu8628 Human PRO
24	2975	96.9	734	6 ABUS8628	Abu8628 Human PRO
25	2975	96.9	734	6 ABUS8628	Abu8628 Human PRO

ALIGNMENTS

RESULT 1

ADC71542

ID ADC71542 standard; protein; 574 AA.

XX AC ADC71542;

XX DT 18-DEC-2003 (first entry)

XX DE Human NOV7b protein SEQ ID NO:170.

XX KW human; NOVx; cytostatic; anorectic; antidiabetic; antiparkinsonian;
KW neuroprotective; neurotropic; immunomodulator; antiarteriosclerotic;
KW nephrotropic; osteopathic; vaccine; gene therapy; cancer; obesity;
KW diabetes; metabolic disorder; anorexia; neurodegenerative disease;
KW Parkinson's disease; Alzheimer's disease; immune disorder;
KW hematopoietic disorder; atherosclerosis; renal failure; hyperkalemia;
KW hypoglycemia; bone disorder; wasting disorder.

XX OS Homo sapiens.

XX PN WO2003040329-A2.

XX PD 15-MAY-2003.

XX PD 05-NOV-2002; 2002WO-US035535.

XX PD 05-NOV-2001; 2001US-0338626P.

XX PD 28-NOV-2001; 2001US-00996015.

XX PD 28-NOV-2001; 2001US-0333912P.

XX PD 29-NOV-2001; 2001US-0334300P.

XX PD 03-DEC-2001; 2001US-0338196P.

XX PD 19-APR-2002; 2002US-0373806P.

XX PD 16-MAY-2002; 2002US-0381043P.

XX PD 07-AUG-2002; 2002US-0401593P.

XX PD 04-NOV-2002; 2002US-00287190.

XX PD (CURA-) CURAGEN CORP.

XX PI Alsobrook JP, Anderson DW, Boldog FL, Burgess CE, Chant JS;

XX PI Chapoval A, Chaudhuri A, Edinger SR, Eisen A, Gangolli EA;

XX PI Gerlach VL, Guo X, Ji W, Khramtsov NV, Leite MW, Li L, Mezes PS;

XX PI Millet I, Ooi CE, Ort T, Padigaru M, Patturajan M, Pena CEA;

XX PI Rastelli L, Rieger DK, Quinn Senger KE, Smithson G, Spaderna SK;

Abu92788 Human sec
Abo08865 Human sec
Abo02917 Human sec
Abr75071 Human sec
Abr94833 Human sec
Abo85806 Human PRO
Abo98966 Novel hum
Abo98181 Novel hum
Abo91887 Novel hum
Abo89580 Human PRO
Abo84421 Human sec
Abo67634 Human sec
Abo80662 Human PRO
Abo99580 Human sec
Abo99870 Human sec
Abo16493 Human sec
Abo92393 Human sec
Abo19034 Human sec
Abo78455 Human sec
Abo85191 Novel hum

PI Chapoval A, Chaudhuri A, Edinger SR, Eisen A, Gangolli EA;
PI Gerlach V, Guo XS, Ji W, Khrantsov NV, Leite MW, Li L, Mezes PS;
PI Millet I, Ooi CE, Ort T, Padigar M, Pattarajan M, Pena CEA;
PI Rastelli L, Rieger DK, Senger KEQ, Smithson G, Spaderna SK;
PI Szytek KA, Stone DJ, Twomlow N, Vernet CAM, Voss EZ, Zerhusen BD;
PI Zhong M;
XX WPI; 2004-213932/20.
DR N-PSDB; ADN33952.
XX Isolated NOVX polypeptides and nucleic acids, useful for preventing,
PT diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
XX Claim 2; SEQ ID NO 170; 129pp; English.
XX The invention relates to 87 isolated NOVX polypeptides (NOV1-NOV5), their
CC mature forms and their encoding polynucleotides having sequence
CC similarity to pancreatic polypeptide (NOV1), angiotensin (NOV2),
CC interleukin-1 (NOV3), endothelin-2 (NOV4), endozepine (NOV5),
CC amphiregulin (NOV6) and metalloproteinase (NOV7). Also included the
CC use of NOVX in the manufacture of a medicament for treating a human
CC disease associated with NOVX, detecting NOVX in a sample via an
CC immunoassay, identifying an agent that binds to the NOVX polypeptide,
CC modulating the activity of NOVX, a vector comprising NOVX polynucleotide,
CC a cell comprising the vector, an antibody that immunospecifically binds
CC to NOVX, detecting the polynucleotide in a sample using a hybridisation
CC assay; and producing the polypeptide comprising culturing the cell under
CC conditions that lead to expression of the polypeptide. NOVX and its
CC polynucleotide are used to prevent, diagnose or treat a medical condition
CC in human related to the aberrant expression and activity of NOVX
CC polypeptides e.g. metabolic disorders, diabetes, obesity, infectious
CC disease, anorexia, cancer, cancer-associated cachexia, neurodegenerative
CC disorders, Alzheimer's disease, Parkinson's disease, immune disorders,
CC haematopoietic disorders, and the various dyslipidaemias, metabolic
CC disturbances associated with obesity, the metabolic syndrome X and
CC wasting disorders associated with chronic diseases and various cancers.
CC They may also be used as antibacterial agents. NOVX may also be used as
CC an antigen in the production of antibodies and in assays to identify
CC modulators (agonists and antagonists) of the expression and activity of
CC NOVX. The present sequence represents a NOVX protein.
XX
SQ Sequence 574 AA;

Query Match 100.0%; Score 3070; DB 8; Length 574;
Best Local Similarity 100.0%; Pred. No. 2.3e-277;
Matches 574; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MWGLLLALAPAPAVGAPALGAPRNSVLGLAQPGTKVPGSTPALHSSPAQPPAETANGTS 60
DB 1 MWGLLLALAPAPAVGAPALGAPRNSVLGLAQPGTKVPGSTPALHSSPAQPPAETANGTS 60
QY 61 EQHVRIRVIKKKVIKKRKKLTLTRETPLVTAGPLVTPPTAGTLDPAEKQETCCPPLGL 120
DB 61 EQHVRIRVIKKKVIKKRKKLTLTRETPLVTAGPLVTPPTAGTLDPAEKQETCCPPLGL 120
QY 121 ESLRVSRLSEASSQSGFLGPHGRNLNIQSGLEDGLYDGAWCAEQDADPWFQVDAGH 180
DB 121 ESLRVSRLSEASSQSGFLGPHGRNLNIQSGLEDGLYDGAWCAEQDADPWFQVDAGH 180
QY 181 PTFPSGVITQGRNSVMRYDWTYSKYQFNSDRFTWGRNSHSSGMDAVFPANSDPTFPVL 240
DB 181 PTFPSGVITQGRNSVMRYDWTYSKYQFNSDRFTWGRNSHSSGMDAVFPANSDPTFPVL 240
QY 241 NLPEPOVARFIRLLPOTLQGGAPCURELACPVSDPDNDLFLFAPASGSSDPLDFQHH 300
DB 241 NLPEPOVARFIRLLPOTLQGGAPCURELACPVSDPDNDLFLFAPASGSSDPLDFQHH 300
QY 301 NYKAMRKLKQVBOQCENITRIYSIGKSYOGLKLYNMESDKPGEHELGEPEVRYVAGMH 360
DB 301 NYKAMRKLKQVBOQCENITRIYSIGKSYOGLKLYNMESDKPGEHELGEPEVRYVAGMH 360
QY 361 GNEALGRELLELLMQFLCHEFRLGRNPRVTRLLESMRIHLLPSMNPDCGYEYAIYHRGSELVG 420
DB 361 GNEALGRELLELLMQFLCHEFRLGRNPRVTRLLESMRIHLLPSMNPDCGYEYAIYHRGSELVG 420

Db 361 GNEALGRELLELLMQFLCHEFRLGRNPRVTRLLESMRIHLLPSMNPDCGYEYAIYHRGSELVG 420
QY 421 WAERWNNQSIDLNHNFPADLNTPLWEAQDDGKVPPIVPHVNHHLPLPTTYTTLPNATVAPETR 480
Db 421 WAERWNNQSIDLNHNFPADLNTPLWEAQDDGKVPPIVPHVNHHLPLPTTYTTLPNATVAPETR 480
QY 481 AVIKWKKRIPFVLISANLHGGLVVSYPFDMVTASAECHSVTRNCRVTFEEGPPPCNFVL 540
Db 481 AVIKWKKRIPFVLISANLHGGLVVSYPFDMVTASAECHSVTRNCRVTFEEGPPPCNFVL 540
QY 541 TKTFKQRLRELLAAGAKVPPDLRRRLERLRGQKD 574
Db 541 TKTFKQRLRELLAAGAKVPPDLRRRLERLRGQKD 574
RESULT 3
AD042303
ID AD042303 standard; protein; 574 AA.
XX
AC AD042303;
DT 15-JUL-2004 (first entry)
XX Human NOVX polypeptide #76.
DE Human; NOVX; cancer; atherosclerosis; diabetes; Alzheimer's disease;
XX Parkinson's disease; graft-versus-host disease; scleroderma;
KW hypertension; haemophilia; idiopathic thrombocytopenic purpura;
KW immunodeficiency; AIDS; dyslipidemia; obesity; Crohn's disease;
KW bronchial asthma; anorexia; cancer-associated cachexia;
KW multiple sclerosis; fertility.
XX Homo sapiens.
XX US2004058338-A1.
XX 25-MAR-2004.
XX 02-DEC-2002; 2002US-00307817.
XX 03-DEC-2001; 2001US-0336881P.
XX 05-DEC-2001; 2001US-0336820P.
XX 07-DEC-2001; 2001US-0338285P.
XX 10-DEC-2001; 2001US-0338318P.
XX 11-DEC-2001; 2001US-0339022P.
XX 11-DEC-2001; 2001US-0339314P.
XX 11-DEC-2001; 2001US-0339516P.
XX 11-DEC-2001; 2001US-0339517P.
XX 11-DEC-2001; 2001US-0339611P.
XX 12-DEC-2001; 2001US-0340981P.
XX 12-DEC-2001; 2001US-0341346P.
XX 14-DEC-2001; 2001US-0340390P.
XX 14-DEC-2001; 2001US-0340440P.
XX 14-DEC-2001; 2001US-0340565P.
XX 14-DEC-2001; 2001US-0340608P.
XX 14-DEC-2001; 2001US-0341144P.
XX 17-DEC-2001; 2001US-0341477P.
XX 17-DEC-2001; 2001US-0341540P.
XX 18-DEC-2001; 2001US-0341768P.
XX 20-DEC-2001; 2001US-0342592P.
XX 31-DEC-2001; 2001US-0344903P.
XX 01-FEB-2002; 2002US-0353286P.
XX 01-FEB-2002; 2002US-0353288P.
XX 26-FEB-2002; 2002US-0359599P.
XX 26-FEB-2002; 2002US-0359626P.
XX 26-FEB-2002; 2002US-0359671P.
XX 27-FEB-2002; 2002US-0359914P.
XX 27-FEB-2002; 2002US-0359956P.
XX 28-FEB-2002; 2002US-0360924P.
XX 28-FEB-2002; 2002US-0360964P.
XX 28-FEB-2002; 2002US-0361028P.
XX 28-FEB-2002; 2002US-0361256P.

28-FEB-2002; 2002US-0361264P.
 05-MAR-2002; 2002US-0361770P.
 05-MAR-2002; 2002US-0362230P.
 13-MAR-2002; 2002US-0364181P.
 13-MAR-2002; 2002US-0364238P.
 15-MAR-2002; 2002US-0364978P.
 15-MAR-2002; 2002US-0365025P.
 17-APR-2002; 2002US-0373288P.
 15-MAY-2002; 2002US-0380981P.
 16-MAY-2002; 2002US-0381004P.
 17-MAY-2002; 2002US-0381495P.
 28-MAY-2002; 2002US-0381534P.
 28-MAY-2002; 2002US-0383744P.
 29-MAY-2002; 2002US-0383829P.
 29-MAY-2002; 2002US-0384024P.
 02-JUL-2002; 2002US-0393312P.
 06-AUG-2002; 2002US-0401315P.
 07-AUG-2002; 2002US-0401788P.
 20-AUG-2002; 2002US-0404676P.
 23-AUG-2002; 2002US-0405400P.
 23-AUG-2002; 2002US-0405684P.
 23-AUG-2002; 2002US-0405687P.
 23-AUG-2002; 2002US-0405698P.
 26-AUG-2002; 2002US-0406353P.
 (AGEE/) AGEE M L.
 (ALSO/) ALSOBOOK J P.
 (ANDE/) ANDERSON D W.
 (BERG/) BERGHS C.
 (BOLD/) BOLDOG F L.
 (BURG/) BURGESS C E.
 (CATT/) CATTERTON E.
 (DIPI/) DIPIPPO V A.
 (EDIN/) EDINGER S R.
 (EISE/) EISEN A.
 (ELLE/) ELLERMAN K.
 (GANG/) GANGOLLI E A.
 (GERL/) GERLACH V.
 (GORM/) GORMAN L.
 (ROTH/) ROTHBERG B G.
 (GUOX/) GUO X S.
 (HERR/) HERMANN J L.
 (HALV/) HALVORSEN Y.
 (JIWU/) JI W.
 (KEKU/) KEKUDA R.
 (KHRA/) KHRAMTSOV N V.
 (LARO/) LAROCHELLE W J.
 (LEPL/) LEPLEY D M.
 (LILL/) LI L.
 (MACD/) MACDUGALL J R.
 (MILL/) MILLER C E.
 (ORTT/) ORT T.
 (PADI/) PADIGARU M.
 (PATT/) PATTURAJAN M.
 (PENA/) PENA C E A.
 (PEYM/) PEYMAN J A.
 (RIEG/) RIEGER D K.
 (ROTH/) ROTHENBERG M E.
 (SHEN/) SHENDY S G.
 (SMIT/) SMITHSON G.
 (SPAD/) SPADERNA S K.
 (SPYT/) SPYTEK K A.
 (STON/) STONE D J.
 (TAUP/) TAUPIER R J.
 (VERN/) VERNET C A M.
 (VOSS/) VOSS E Z.
 (ZHON/) ZHONG M.
 Agee ML, Alsbrook JP, Anderson DM, Berghs C, Boldog FL,
 Burgess CE, Catterton E, Dipippo VA, Edinger SR, Eisen A,
 Ellerman K, Gangolli EA, Gerlach V, Gorman L, Rothberg BG,
 Herrmann JL, Halvorsen Y, Ji W, Kekuda R, Khrantsov NV,
 Larochelle WJ, Lepley DM, Li L, Macdougall JR, Miller CE, Ort T,

PI Padigaru M, Patturajan M, Pena CEA, Peyman JA, Rieger DK,
 Rothenberg ME, Shenoy SG, Smithson G, Spaderna SK, Spytek KA,
 Stone DJ, Taupier RU, Vernet CAM, Voss EZ, Zhong M,
 WPI; 2004-268786/25.
 DR N-PSDB; ADO42302.
 XX
 PT New human NOVX polypeptides and nucleic acid molecules, useful for
 diagnosing, preventing or treating NOVX-associated disorder, e.g. cancer,
 atherosclerosis, diabetes, Alzheimer's disease, Parkinson's disease or
 scleroderma.
 PT
 XX
 PS Claim 1; SEQ ID NO 152; 610pp; English.
 CC
 CC The invention relates to human NOVX polypeptides and the polynucleotides
 encoding them. The invention also relates to antibodies specific to the
 NOVX polypeptides. The polypeptides, polynucleotides and antibodies are
 useful for manufacturing a medicament for treating a syndrome associated
 with a human disease, such as a pathology associated with the NOVX
 polypeptide. The sequences are useful for diagnosing, treating or
 preventing a NOVX-associated disorder, e.g., cancer, atherosclerosis,
 diabetes, Alzheimer's disease, Parkinson's disease, graft-versus-host
 disease, scleroderma, immunodeficiencies, AIDS, dyslipidemia,
 thrombocytopenic purpura, hypertension, haemophilia, idiopathic
 obesity, Crohn's disease, bronchial asthma, anorexia, cancer-associated
 cachexia, multiple sclerosis or fertility. The nucleic acids may be used
 as hybridisation probes, in chromosome mapping, in tissue typing, in
 preventive medicine or in pharmacogenomics. This sequence represents a
 human NOVX polypeptide of the invention.
 CC
 XX Sequence 574 AA;
 SQ

Query Match 100.0%; Score 3070; DB 8; Length 574;
 Best Local Similarity 100.0%; Pred. No. 2.3e-277;
 Matches 574; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MWGLLALAPAVGALGAPRNSVLGLAQPGTKVPGSTPALHSSPAQPAETANGTS 60
 DB 1 MWGLLALAPAVGALGAPRNSVLGLAQPGTKVPGSTPALHSSPAQPAETANGTS 60
 QY 61 EQHVRIRVIRKKKVIIMKKRKLTLTRPTPLVLTAGPLVTPAGTLDPAEKQETCCPLGL 120
 DB 61 EQHVRIRVIRKKKVIIMKKRKLTLTRPTPLVLTAGPLVTPAGTLDPAEKQETCCPLGL 120
 QY 121 ESLRVSDSLRLASSSQSGFLGPHRGRNLNIOGLEDGLDYGAWCAEQDADPWQVDAGH 180
 DB 121 ESLRVSDSLRLASSSQSGFLGPHRGRNLNIOGLEDGLDYGAWCAEQDADPWQVDAGH 180
 QY 181 PTRFSGVITQGRNSVMRYDWTYSYKVFNSDRTWGRNSHSSGMDAVFPANSDPETPVL 240
 DB 181 PTRFSGVITQGRNSVMRYDWTYSYKVFNSDRTWGRNSHSSGMDAVFPANSDPETPVL 240
 QY 241 NLLPEQVAFIRLLPOTWLQGGAPCLRAEILACPVSDPNDLFLAPASGSDPLDFQHH 300
 DB 241 NLLPEQVAFIRLLPOTWLQGGAPCLRAEILACPVSDPNDLFLAPASGSDPLDFQHH 300
 QY 301 NYKAMRKLKMQVQEQCPNITRIYSIGKSYQGLKLYVMEMSDKGEHELGEPEVRYVAGMH 360
 DB 301 NYKAMRKLKMQVQEQCPNITRIYSIGKSYQGLKLYVMEMSDKGEHELGEPEVRYVAGMH 360
 QY 361 GNEALGRELLLLMQFLCHFEFLRGNPRVTRLLSEMIHLLPSMNPDGYEIAYHRGSELVG 420
 DB 361 GNEALGRELLLLMQFLCHFEFLRGNPRVTRLLSEMIHLLPSMNPDGYEIAYHRGSELVG 420
 QY 421 WAEGRWNNQSIDLNHNFDNLTPLWEAQDDGKVPHIVPNHHLPTTYTLPNATVAPETR 480
 DB 421 WAEGRWNNQSIDLNHNFDNLTPLWEAQDDGKVPHIVPNHHLPTTYTLPNATVAPETR 480
 QY 481 AVIKWMKRIPFVLNANLHGGELVSYPFQDMVTASAEYHSVTRNCRVTFEEGPPFCNPFVL 540
 DB 481 AVIKWMKRIPFVLNANLHGGELVSYPFQDMVTASAEYHSVTRNCRVTFEEGPPFCNPFVL 540
 QY 541 TKTPKQRLRELLAAGAKVPPDLRRRLRLRGQKD 574

PI Agarwal P, Murdoch PR, Rizvi SK, Smith RF, Xiang Z, Kabnick KS;
 PI Lai Y;
 XX WPI; 2001-639223/73.
 DR N-PSDB; AA167207.
 XX Isolated polypeptides, which may be peptide hormones, which are
 PT identified by high throughput genome-based biology which identifies genes
 PT and gene products as therapeutic targets for treatment of diseases such
 PT as diabetes and cancer.
 XX Claim 1; Page 97-98; 99pp; English.
 CC The invention provides polypeptides (AAG65886-65918) which may be peptide
 CC hormone (including insulin, growth hormones, chemokines, cytokines,
 CC neuropeptides, integrins, kallikreins, lamins, melanins, natriuretic
 CC hormones, neurotensin, pituitary hormones, pleiotrophins, prostaglandin,
 CC acetylcholine, selectins, thromboglobulin, thymosin) identified by
 CC high throughput genome-based biology and polynucleotides (AA167176-67201)
 CC encoding them. The polypeptides can be expressed by standard recombinant
 CC methodology. The polypeptides are useful in the treatment of disease such
 CC as diabetes, breast, prostate, colon cancer and other malignant tumor,
 CC hyper- and hypotension, obesity, bulimia, anorexia, growth abnormalities,
 CC asthma, manic depression, dementia, delirium, mental retardation,
 CC Huntington's disease, Tourette's syndrome, schizophrenia, growth, mental
 CC or sexual development disorders, and dysfunctions of the blood cascade
 CC system including those leading to stroke. The polynucleotides may be used
 CC as diagnostic reagents through detecting mutations in the associated genes
 CC and for chromosome localization and for tissue expression studies. The
 CC polypeptides and polynucleotides may also be used as vaccines
 XX Sequence 734 AA;

Query Match 97.18; Score 2980; DB 4; Length 734;
 Best Local Similarity 78.28; Pred No 9e-269; 0; Mismatches 160; Gaps 1;
 Matches 574; Conservative 0;
 1 MWGILLALAFAPAVGALCAPNSVLGLAORCTTKVPGSTPALHSSPAQPAETANGTS 6
 1 MWGILLALAFAPAVGALCAPNSVLGLAORCTTKVPGSTPALHSSPAQPAETANGTS 6
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 61 EOHVRIRIVIKKKVIMKKRKLTLTPPLVTAAGPLVTPACTLDPAEKQETGCPPLGL 1.0
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 121 ESLRVSDSRLEASSOSFGLGPHRGINTOSGLEDDLYDGAWCAEQDADPWFQVDAGH 1.0
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 181 PTFPSGVITQGRNSVVRVYDVTYKYVQFNSDRTWGSNHSCHDVPFANSDETPVL 2.0
 241 NLLPEQVAFETLIPOTWLOGCAPCLRAEILACPVSDNDLFLFAPASGSDPLDFQHH 3.0
 241 NLLPEQVAFETLIPOTWLOGCAPCLRAEILACPVSDNDLFLFAPASGSDPLDFQHH 3.0
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 301 NYKAMRKLKMOVQCPNITRIYSGKSYQGLKLYMMSDLPGBHEIGEPEVRVYAGMH 3.0
 361 GNEALGRELILLIMQFLCHEFLRCHPRVTRLLSEMRHLLPSMNDPGVEIAYHRSSELV 4.0
 361 GNEALGRELILLIMQFLCHEFLRCHPRVTRLLSEMRHLLPSMNDPGVEIAYHRSSELV 4.0
 421 WAEGRWNNOSIDLNHFADNLPLEAQQDKVPHIVPNHHLPLPTYYTLFNATVAPETR 4E
 421 WAEGRWNNOSIDLNHFADNLPLEAQQDKVPHIVPNHHLPLPTYYTLFNATVAPETR 4E
 481 AVIKWKKRTPVLSANLHGGELVYSPDP-----50
 481 AVIKWKKRTPVLSANLHGGELVYSPDPDMTRTPWAARELTFTPDPAVFRWLSTVYAGSN 54

QY 510 ----- 509
 Db 541 LAMQDTSRRPCHSQDSFVHGNIINGADMHTVPGSMNDFSYLHNCFEVTVLSCKDFPHE 600
 QY 510 ----- 509
 Db 601 NELPQEWENKDALITYLEQVRMGVAGVVRDKDTBELGIADAVIADGINHDVTTAWGGDY 660
 QY 510 -----MYTASAEVHVSVTRNCRVTFEEGPFPCNFVLTPTKQRLRELLAAGAKVPP 560
 Db 661 WRLLTPGDYMWVTASAEVHVSVTRNCRVTFEEGPFPCNFVLTPTKQRLRELLAAGAKVPP 720
 QY 561 DLRRRLRLRGOKD 574
 Db 721 DLRRRLRLRGOKD 734
 RESULT 6
 ID ADC71546
 ID ADC71546 standard; protein, 734 AA.
 XX ADC71546;
 AC ADC71546;
 DT 18-DEC-2003 (first entry)
 DE Human NOV7d protein SEQ ID NO:174.
 XX human; NOVX; cytostatic; anorectic; antidiabetic; antiparkinsonian;
 KW neuroprotective; neotropic; immunomodulator; antiarteriosclerotic;
 KW nephrotropic; osteopathic; vaccine; gene therapy; cancer; obesity;
 KW diabetes; metabolic disorder; anorexia; neurodegenerative disease;
 KW Parkinson's disease; Alzheimer's disease; immune disorder;
 KW haematopoietic disorder; atherosclerosis; renal failure; hyperkalaemia;
 KW hypoglycaemia; bone disorder; wasting disorder.
 XX Homo sapiens.
 OS WO2003040329-A2.
 XX PD 15-MAY-2003.
 XX 05-NOV-2002; 2002WO-US035535.
 XX 05-NOV-2001; 2001US-0338626P.
 PR 28-NOV-2001; 2001US-00996015.
 PR 29-NOV-2001; 2001US-033912P.
 PR 03-DEC-2001; 2001US-0334300P.
 PR 19-APR-2002; 2001US-0338196P.
 PR 16-MAY-2002; 2002US-0373806P.
 PR 07-AUG-2002; 2002US-0381043P.
 PR 04-NOV-2002; 2002US-0401593P.
 (CURA-) CURAGEN CORP.
 PI Alsbrook JP, Anderson DW, Boldog FL, Burgess CE, Chant JS;
 PI Chapoval A, Chaudhuri A, Edinger SR, Eisen A, Gangolli EA;
 PI Gerlach VL, Guo X, Ji W, Khrantsov NV, Leite MW, Li L, Mezes PS;
 PI Millet I, Ooi CE, Ort T, Padigaru M, Patturajan M, Pena CE;
 PI Rastelli L, Rieger DK, Quinn Senger KE, Smithson G, Spaderna SK;
 PI Spytek KA, Stone DJ, Twinclo N, Vernet CM, Voss EZ, Zerhusen BD;
 XX Zhong M;
 WPI; 2003-441554/41.
 N-PSDB; ADC71545.
 XX New NOVX polypeptides and nucleic acids for diagnosing, preventing or
 PT treating NOVX-associated disorders, e.g. cancer, obesity, diabetes or
 PT atherosclerosis, and for chromosome mapping, tissue typing or
 PT pharmacogenomics.
 XX Claim 1; SEQ ID NO 174; 112pp; English.

CC The present invention describes novel human proteins designated NOVX,
CC where X can be an integer of 1 to 7. The NOVX protein and nucleotide
CC sequences have cytostatic, anorectic, antidiabetic, antiparkinsonian,
CC neuroprotective, neurotropic, immunomodulator, antiarteriosclerotic,
CC nephrotropic and osteopathic activities, and can be used in vaccines and
CC in gene therapy. The NOVX proteins can be used in manufacturing a
CC medicament for treating a syndrome associated with a human disease, the
CC disease selected from a pathology associated with the protein. The
CC disease can be cancer. NOVX proteins, nucleic acid molecules and
CC antibodies may also be used for diagnosing, treating or preventing other
CC pathologies associated with aberrant NOVX expression or activity, such as
CC obesity, diabetes, metabolic disorders, anorexia, neurodegenerative
CC diseases (e.g. Parkinson's disease or Alzheimer's disease), immune
CC disorders, haematopoietic disorders, atherosclerosis, renal failure,
CC hyperkalaemia, hypoglycaemia, bone disorders and wasting disorders. The
CC NOVX nucleic acids and proteins may also be used in chromosome mapping,
CC tissue typing, predictive medicine and pharmacogenomics. The present
CC sequence is used in the exemplification of the present invention. N.B.
CC The present sequence is designated SEQ ID NO:174, but does not correspond
CC with the sequence of SEQ ID NO:174 given on page 179.
XX
SQ Sequence 734 AA;

Query Match 97.1%; Score 2980; DB 7; Length 734;
Best Local Similarity 78.2%; Pred. No. 9e-269;
Matches 574; Conservative 0; Mismatches 0; Indels 160; Gaps 1;

QY 1 MWGILLALAPAVGALGAPRNSVLGLAQGTGKVPSTPALHSSPAQPPAETANGTS 60
DB 1 MWGILLALAPAVGALGAPRNSVLGLAQGTGKVPSTPALHSSPAQPPAETANGTS 60
QY 61 EQHVIRIVIKKKVIMKKRKKLTTRTPTPLVTAGTLPVTPAGTLDPAEKQETGCPPLGL 120
DB 61 EQHVIRIVIKKKVIMKKRKKLTTRTPTPLVTAGTLPVTPAGTLDPAEKQETGCPPLGL 120
QY 121 ESLRVSRLSEASSQSGFLGPHGRNLNIOGLEDGLYDGAWCAEQDADPWFQVDAGH 180
DB 121 ESLRVSRLSEASSQSGFLGPHGRNLNIOGLEDGLYDGAWCAEQDADPWFQVDAGH 180
QY 181 PTRFSGVITQGRNSVRWYDWTSTKVQFSDNSRTWGRNSHSSGMDAVFPANSDPETPVL 240
DB 181 PTRFSGVITQGRNSVRWYDWTSTKVQFSDNSRTWGRNSHSSGMDAVFPANSDPETPVL 240
QY 241 NLLPEQVAFIRLLPQTWLGGAAPCLRAELTACVSDPNDLFLFAPASGSSDPLDFQHH 300
DB 241 NLLPEQVAFIRLLPQTWLGGAAPCLRAELTACVSDPNDLFLFAPASGSSDPLDFQHH 300
QY 301 NYKAMRKLKQVQPCNITRIYSIGKSYQGLKLYVMEMSDKPGHEHGLGPEVRYVAGMH 360
DB 301 NYKAMRKLKQVQPCNITRIYSIGKSYQGLKLYVMEMSDKPGHEHGLGPEVRYVAGMH 360
QY 361 GNEALGRELILLMOFLCHFLRGNPRVTRLISMRTHLLPSMNPDCGYETAYHRGSELVG 420
DB 361 GNEALGRELILLMOFLCHFLRGNPRVTRLISMRTHLLPSMNPDCGYETAYHRGSELVG 420
QY 421 WAEGRWNNQSIDLNHNFADLNTPLWEAQDDQKVPVHVPVNHHLPLPTYTYLTPNATVAPETR 480
DB 421 WAEGRWNNQSIDLNHNFADLNTPLWEAQDDQKVPVHVPVNHHLPLPTYTYLTPNATVAPETR 480
QY 481 AVIKWKKRIIPFVLSANLHGSELVVSYPFD----- 509
DB 481 AVIKWKKRIIPFVLSANLHGSELVVSYPFDTRTPWAARELTPTDDAVFRWLSTVYAGSN 540
QY 510 ----- 509
DB 541 LAMQDTSRRPCHSQDFSVHGNINGADMTVPVGMNDFSYLHTNCFEVTVELSCDKFPHE 600
QY 510 ----- 509
DB 601 NELPQWENNKDALLTYLEQVRMGVAGVVRDKDTLGIADAVTAVDGINHDVTWAGGDY 660
QY 510 -----MVTASAGYHSVTRNCRVTFEBGPPFCNFVLTQPKQRLRELLAAGAKVPP 560
|||||

DB 661 WRLLTGDMVTASAGYHSVTRNCRVTFEBGPPFCNFVLTQPKQRLRELLAAGAKVPP 720
QY 561 DLRRERLERLRGQKD 574
DB 721 DLRRLERLRGQKD 734
RESULT 7
ID ADC71540 standard; protein; 734 AA.
XX AC ADC71540;
XX DT 18-DEC-2003 (first entry)
XX DE Human NOV7a protein SEQ ID NO:168.
XX KW human; NOVX; cytostatic; anorectic; antidiabetic; antiparkinsonian;
KW neuroprotective; neurotropic; immunomodulator; antiarteriosclerotic;
KW nephrotropic; osteopathic; vaccine; gene therapy; cancer; obesity;
KW diabetes; metabolic disorder; anorexia; neurodegenerative disease;
KW Parkinson's disease; Alzheimer's disease; immune disorder;
KW haematopoietic disorder; atherosclerosis; renal failure; hyperkalaemia;
KW hypoglycaemia; bone disorder; wasting disorder.
XX OS Homo sapiens.
XX PN W02003040329-A2.
XX PD 15-MAY-2003.
XX PF 05-NOV-2002; 2002WO-US035535.
XX PR 05-NOV-2001; 2001US-0338626P.
XX PR 28-NOV-2001; 2001US-00996015.
XX PR 29-NOV-2001; 2001US-0333912P.
XX PR 03-DEC-2001; 2001US-0334300P.
XX PR 19-APR-2002; 2002US-0338196P.
XX PR 16-MAY-2002; 2002US-0373806P.
XX PR 16-MAY-2002; 2002US-0381043P.
XX PR 04-AUG-2002; 2002US-0401593P.
XX PR 04-NOV-2002; 2002US-00287190.
XX (CURA-) CURAGEN CORP.
XX Alsobrook JP, Anderson DW, Boldog FL, Burgess CE, Chant JS;
XX Chapoval A, Chaudhuri A, Binger SR, Eissen A, Gangolli EA;
XX Gerlach VL, Guo X, Ji W, Khrantsov NV, Leite MW, Li L, Mezes PS;
XX Millet I, Ooi CE, Ort T, Padigaru M, Patturajan M, Pena CEA;
XX Rastelli L, Rieger DK, Quinn Senger KE, Smithson G, Spaderna SK,
XX Spytek KA, Stone DJ, Twomlow N, Vernet CAM, Voss EZ, Zerhusen BD;
XX Zhong M;
XX WPI; 2003-441554/41.
XX N-PSDB; ADC71539.
XX New NOVX polypeptides and nucleic acids for diagnosing, preventing or
XX treating NOVX-associated disorders, e.g. cancer, obesity, diabetes or
XX atherosclerosis, and for chromosome mapping, tissue typing or
XX pharmacogenomics.
XX Claim 1; SEQ ID NO 168; 112pp; English.
XX The present invention describes novel human proteins designated NOVX,
XX where X can be an integer of 1 to 7. The NOVX protein and nucleotide
XX sequences have cytostatic, anorectic, antidiabetic, antiparkinsonian,
XX neuroprotective, neurotropic, immunomodulator, antiarteriosclerotic,
XX nephrotropic and osteopathic activities, and can be used in vaccines and
XX in gene therapy. The NOVX proteins can be used in manufacturing a
XX medicament for treating a syndrome associated with a human disease, the
XX disease selected from a pathology associated with the protein. The
XX disease can be cancer. NOVX proteins, nucleic acid molecules and
XX antibodies may also be used for diagnosing, treating or preventing other

pathologies associated with aberrant NOVX expression or activity, such as obesity, diabetes, metabolic disorders, anorexia, neurodegenerative diseases (e.g. Parkinson's disease or Alzheimer's disease), immune disorders, hematopoietic disorders, atherosclerosis, renal failure, hyperkalemia, hypoglycaemia, bone disorders and wasting disorders. The NOVX nucleic acids and proteins may also be used in chromosome mapping, tissue typing, predictive medicine and pharmacogenomics. The present sequence is used in the exemplification of the present invention.

XX Sequence 734 AA;

Query Match 97.1%; Score 2980; DB 7; Length 734;
 Best Local Similarity 78.2%; Pred. No. 9e-269;
 Matches 574; Conservative 0; Mismatches 0; Indels 160; Gaps 1;
 Qy 1 MWGLLLAALAFAPAVGALGAPNSVLGLAOPGTTKVPGSTPALHSSPAOPPAETANGTS ()
 Db 1 MWGLLLAALAFAPAVGALGAPNSVLGLAOPGTTKVPGSTPALHSSPAOPPAETANGTS ()
 Qy 61 EOHVIRIVIKKKVIMKKRKLTLTRPTPLVTAGPLVTPPAAGTLPAAEKQETGCPPLGL 1 10
 Db 61 EOHVIRIVIKKKVIMKKRKLTLTRPTPLVTAGPLVTPPAAGTLPAAEKQETGCPPLGL 1 10
 Qy 121 ESLVSDSRLEASSQSGFLGPHRGRNLIOGLEDGLYDGAWCAEQDADPMFQVDAGH 1 10
 Db 121 ESLVSDSRLEASSQSGFLGPHRGRNLIOGLEDGLYDGAWCAEQDADPMFQVDAGH 1 10
 Qy 181 PTPSGVITGRNSVWRDYDVTYKQFNSDRTWMSRHHSGMDAVFPANSDPETPYL 2 10
 Db 181 PTPSGVITGRNSVWRDYDVTYKQFNSDRTWMSRHHSGMDAVFPANSDPETPYL 2 10
 Qy 241 NLLPEQVAFIRLLPOTMLOGGAPCLRAILACPVSDNDLPLEAPASGSDPLDFOHH 3 10
 Db 241 NLLPEQVAFIRLLPOTMLOGGAPCLRAILACPVSDNDLPLEAPASGSDPLDFOHH 3 10
 Qy 301 NYKAMRKLKMQVOQCPNTRIYSIGKSYOGLKLYMEMSDRPEGEHELGEPEVRYVAGMH 3 10
 Db 301 NYKAMRKLKMQVOQCPNTRIYSIGKSYOGLKLYMEMSDRPEGEHELGEPEVRYVAGMH 3 10
 Qy 361 GNEALGRELLLLMQFLCHEFLGNRPVTRLLESEMIRHLLPSMNPDPGYEIAHRGSELVG 4 0
 Db 361 GNEALGRELLLLMQFLCHEFLGNRPVTRLLESEMIRHLLPSMNPDPGYEIAHRGSELVG 4 0
 Qy 421 WAEGRWNNOSIDLNNHPADLNTPLWBAODDGKVPHTVPNNHLLPLPTTYTLPNATVAPETR 4 0
 Db 421 WAEGRWNNOSIDLNNHPADLNTPLWBAODDGKVPHTVPNNHLLPLPTTYTLPNATVAPETR 4 0
 Qy 481 AVIKWMKRIPFVLSANLHGELVSYFPD----- 5 9
 Db 481 AVIKWMKRIPFVLSANLHGELVSYFPD----- 5 9
 Qy 510 ----- 5 9
 Db 510 ----- 5 9
 Qy 541 LAMQDTSRRPCHSQDSVHGNIIINGADWHTVPGSMNDFSYLHTNCFEVTVELSCDKFPHE 6 0
 Db 510 ----- 5 9
 Qy 601 NELPOEWENNKDALLTYLEQVRMGIAGVVRDKDTELGIADAVIADVGINHDVTTAWGGDY 6 0
 Qy 510 -----MVTASAGYHSVTRNCRVTPTEGPFPCNFVLTTPKQRLRELLAAGAKVPP 5 0
 Db 661 WRLLTPGDVMTASAGYHSVTRNCRVTPTEGPFPCNFVLTTPKQRLRELLAAGAKVPP 7 0
 Qy 561 DLRRRLRLRGOKD 574
 Db 721 DLRRRLRLRGOKD 734

RESULT 8

ID ADP65320 standard; protein; 734 AA.

XX AC ADP65320;

XX DT 12-AUG-2004 (first entry)
 DE Human metallocarboxypeptidase cpx-1.
 XX
 KW autoimmune disease; arthritis; gene expression analysis;
 KW rheumatoid arthritis; collagen-induced; immunosuppressive; anti-rheumatic;
 KW antirheumatic; osteopathic; antigout; antiinflammatory; dermatological;
 KW immunomodulatory; lupus; ankylosing spondylitis; Fibrositis;
 KW fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;
 KW immune; human.
 XX
 OS Homo sapiens.
 XX WO2003072827-A1.
 XX 04-SEP-2003.
 XX 31-OCT-2002; 2002WO-US035433.
 XX 31-OCT-2001; 2001US-0336220P.
 XX (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
 PA Hirsch R, Thorton SL;
 PI WPI: 2003-712740/67.
 XX GENBANK; NP_062555.
 PT Diagnosing and analyzing autoimmune disease using gene expression
 PT profiles and microarray technology, useful for diagnosing and treating
 PT rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and
 XX gout.
 PS Disclosure; Page; 56pp; English.

The invention relates to a novel method for diagnosing and analysing autoimmune disease or arthritides. The method comprises obtaining a patient sample containing mRNA, analysing gene expression using the mRNA that results in a gene expression signature of the mRNA, and using that gene expression signature to diagnose or analyse the autoimmune disease or arthritides in the patient, where gene expression of at least 60% of the genes correlates with that of the gene signature. The invention further comprises a treatment of rheumatoid arthritis. Identification of genes for targeting in the treatment of rheumatoid arthritis in a mammal other than a mouse; diagnosis of rheumatoid arthritis in a mammal; an array or gene chip, specific for rheumatoid arthritis; screening or analyses of autoimmune disease or rheumatoid arthritis; diagnosing the efficacy of a candidate drug in vitro for the treatment of collagen-induced arthritis; and reducing the symptoms associated with collagen-induced arthritis. The compositions of the invention have the following activities: immunosuppressive, anti-rheumatic, antiarthritic, osteopathic, antigout, antiinflammatory, dermatological, and immunomodulatory. The methods and compositions of the present invention are useful for diagnosing and treating autoimmune disease or arthritides, such as rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis, fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and immune disease caused by an infectious agent. This sequence represents a protein sequence relating to the genes used in the analysis and treatment of autoimmune diseases or arthritides. Note: This sequence is not shown in the specification. It has been supplied in an electronic format from WIPO.

XX SQ Sequence 734 AA;

Query Match 97.1%; Score 2980; DB 7; Length 734;
 Best Local Similarity 78.2%; Pred. No. 9e-269;
 Matches 574; Conservative 0; Mismatches 0; Indels 160; Gaps 1;

Qy 1 MWGLLLAALAFAPAVGALGAPNSVLGLAOPGTTKVPGSTPALHSSPAOPPAETANGTS 60

Db 1 MWGLLLAALAFAPAVGALGAPNSVLGLAOPGTTKVPGSTPALHSSPAOPPAETANGTS 60

to NOVX, detecting the polynucleotide in a sample using a hybridization assay; and producing the polypeptide comprising culturing the cell under conditions that lead to expression of the polypeptide. NOVX and its polynucleotide are used to prevent, diagnose or treat a medical condition in human related to the aberrant expression and activity of NOVX polypeptides e.g. metabolic disorders, diabetes, obesity, infectious disease, anorexia, cancer, cancer-associated cachexia, neurodegenerative disorders, Alzheimer's disease, Parkinson's disease, immune disorders, haematopoietic disorders, and the various dyslipid, metabolic and wasting disorders associated with obesity, the metabolic syndrome X and They may also be used as antibacterial agents. NOVX may also be used as an antigen in the production of antibodies and in assays to identify modulators (agonists and antagonists) of the expression and activity of NOVX. The present sequence represents a NOVX protein.

Sequence 734 AA;

Query Match		97.1%; Score 2980; DB 8; Length 734;
Best Local Similarity		78.2%; Pred. No. 9e-269; 0; Mismatches 160; Gaps 1;
Matches 574; Conservative		0; Mismatches 160; Gaps 1;
QY	1	MWGLLLAALAPAPAVGALGAPNSVLGLAQPCTTKVPGSTPAHSHSPAQPPAETANGTS 6
DB	1	MWGLLLAALAPAPAVGALGAPNSVLGLAQPCTTKVPGSTPAHSHSPAQPPAETANGTS 6
QY	61	EOHVRIRVKKKVIKKKILTRPTPLVATAGPLVTPAGTLDPAEKQETGCPPLGL 1 0
DB	61	EOHVRIRVKKKVIKKKILTRPTPLVATAGPLVTPAGTLDPAEKQETGCPPLGL 1 0
QY	121	ESLRVDSRLSEASSQFGLPHRGRLNTQSLGDLVDGAWCAEQADPWFQVDAGH 1 0
DB	121	ESLRVDSRLSEASSQFGLPHRGRLNTQSLGDLVDGAWCAEQADPWFQVDAGH 1 0
QY	181	PTPSGVITQGRNVHRYDWTYSKYQFNSDSTWGSNRHSSGMDAVFPANSDPDPVL 2 0
DB	181	PTPSGVITQGRNVHRYDWTYSKYQFNSDSTWGSNRHSSGMDAVFPANSDPDPVL 2 0
QY	241	NILPEQVAFIRILLPOTNLQGGAPCLRAIFILACPVSDPNDLFLAPASGSDPLDFQHH 3 0
DB	241	NILPEQVAFIRILLPOTNLQGGAPCLRAIFILACPVSDPNDLFLAPASGSDPLDFQHH 3 0
QY	301	NYKAMKLMKQVQECQPNTRIYSIGSKYQGLKLYWEMSDKPGHGEPEVRYVAGWH 3 0
DB	301	NYKAMKLMKQVQECQPNTRIYSIGSKYQGLKLYWEMSDKPGHGEPEVRYVAGWH 3 0
QY	361	GNEALGRELILLMQLCHEFLRGNPRVTRLLSEMRHLLPSMNDPGVEIAYHRSSELVG 4 0
DB	361	GNEALGRELILLMQLCHEFLRGNPRVTRLLSEMRHLLPSMNDPGVEIAYHRSSELVG 4 0
QY	421	WAEGRWNNQSIDLNNFADLNTPLWEAQDDGKVPHIVPNHHLPPLTYTLPNATVAPETR 4 0
DB	421	WAEGRWNNQSIDLNNFADLNTPLWEAQDDGKVPHIVPNHHLPPLTYTLPNATVAPETR 4 0
QY	481	AVIKKWKRIPTVLSANLHGGELVWSYPPD----- 50
DB	481	AVIKKWKRIPTVLSANLHGGELVWSYPPD----- 50
QY	510	----- 50
DB	510	----- 50
QY	541	LAMQDTSRRPCHQSDFSVHGNINGADMHTVPGSMNDFSYLHTRNCFEVTVELSCDKFHE 60
DB	541	LAMQDTSRRPCHQSDFSVHGNINGADMHTVPGSMNDFSYLHTRNCFEVTVELSCDKFHE 60
QY	601	NELPOEWENNKDALLTYLEQVRNAGVVRDKUTELGIADAVIAVDGINHDVTTAWGGDY 66
DB	601	NELPOEWENNKDALLTYLEQVRNAGVVRDKUTELGIADAVIAVDGINHDVTTAWGGDY 66
QY	661	WLLFTPGDYMWVASAGVSHVTRNCRVTFEEGPPFCNFVLTPTKQRLRELLAAGAKVPP 56
DB	661	WLLFTPGDYMWVASAGVSHVTRNCRVTFEEGPPFCNFVLTPTKQRLRELLAAGAKVPP 56
QY	721	DURRLERLRGOKD 574
DB	721	DURRLERLRGOKD 574

RESULT 10	
ADO42301	
ID	ADO42301 standard; protein; 734 AA.
XX	ADO42301;
XX	15-JUL-2004 (first entry)
XX	Human NOVX polypeptide #75.
XX	Human; NOVX; cancer; atherosclerosis; diabetes; Alzheimer's disease; Parkinson's disease; graft-versus-host disease; scleroderma; hypertension; haemophilia; idiopathic thrombocytopenic purpura; immunodeficiency; AIDS; dyslipidemia; obesity; Crohn's disease; bronchial asthma; anorexia; cancer-associated cachexia; multiple sclerosis; fertility.
XX	Homo sapiens.
XX	US2004058338-A1.
XX	25-MAR-2004.
XX	02-DEC-2002; 2002US-00307817.
XX	03-DEC-2001; 2001US-0336881P.
XX	05-DEC-2001; 2001US-0336820P.
XX	07-DEC-2001; 2001US-0338285P.
XX	10-DEC-2001; 2001US-0338318P.
XX	10-DEC-2001; 2001US-0338989P.
XX	11-DEC-2001; 2001US-0339022P.
XX	11-DEC-2001; 2001US-0339314P.
XX	11-DEC-2001; 2001US-0339516P.
XX	11-DEC-2001; 2001US-0339517P.
XX	11-DEC-2001; 2001US-0339611P.
XX	12-DEC-2001; 2001US-0340981P.
XX	12-DEC-2001; 2001US-0341346P.
XX	14-DEC-2001; 2001US-0340390P.
XX	14-DEC-2001; 2001US-0340440P.
XX	14-DEC-2001; 2001US-0340565P.
XX	14-DEC-2001; 2001US-0340608P.
XX	17-DEC-2001; 2001US-0341147P.
XX	17-DEC-2001; 2001US-0341540P.
XX	18-DEC-2001; 2001US-0341768P.
XX	20-DEC-2001; 2001US-0342592P.
XX	31-DEC-2001; 2001US-034903P.
XX	01-FEB-2002; 2002US-0353286P.
XX	01-FEB-2002; 2002US-0353288P.
XX	26-FEB-2002; 2002US-0359599P.
XX	26-FEB-2002; 2002US-0359626P.
XX	26-FEB-2002; 2002US-0359671P.
XX	27-FEB-2002; 2002US-0359914P.
XX	27-FEB-2002; 2002US-0359956P.
XX	28-FEB-2002; 2002US-0360924P.
XX	28-FEB-2002; 2002US-0360964P.
XX	28-FEB-2002; 2002US-0361028P.
XX	28-FEB-2002; 2002US-0361256P.
XX	28-FEB-2002; 2002US-0361264P.
XX	05-MAR-2002; 2002US-0361770P.
XX	13-MAR-2002; 2002US-0362230P.
XX	13-MAR-2002; 2002US-0364181P.
XX	13-MAR-2002; 2002US-0364238P.
XX	15-MAR-2002; 2002US-0364978P.
XX	17-APR-2002; 2002US-0365025P.
XX	15-MAY-2002; 2002US-0373288P.
XX	16-MAY-2002; 2002US-0380981P.
XX	17-MAY-2002; 2002US-0381004P.
XX	17-MAY-2002; 2002US-0381495P.
XX	28-MAY-2002; 2002US-0383534P.
XX	28-MAY-2002; 2002US-0383744P.

PR 29-MAY-2002; 2002US-0383829P.
 PR 29-MAY-2002; 2002US-0384024P.
 PR 02-JUL-2002; 2002US-0393332P.
 PR 06-AUG-2002; 2002US-0401315P.
 PR 07-AUG-2002; 2002US-041788P.
 PR 20-AUG-2002; 2002US-0404676P.
 PR 23-AUG-2002; 2002US-0405400P.
 PR 23-AUG-2002; 2002US-0405684P.
 PR 23-AUG-2002; 2002US-0405687P.
 PR 23-AUG-2002; 2002US-0405698P.
 PR 26-AUG-2002; 2002US-0406353P.
 XX (AGEE//) AGEE M L.
 PA (ALSO//) ALBROOK J P.
 PA (ANDE//) ANDERSON D W.
 PA (BERG//) BERGHS C.
 PA (BOLD//) BOLDOG F L.
 PA (BURG//) BURGESS C E.
 PA (CATT//) CATTERTON E.
 PA (DIP//) DIPIPPO V A.
 PA (EDIN//) EDINGER S R.
 PA (EISE//) EISEN A.
 PA (ELLE//) ELLERMAN K.
 PA (GANG//) GANGOLLI E A.
 PA (GERL//) GERLACH V.
 PA (GORM//) GORMAN L.
 PA (ROTH//) ROTHBERG B G.
 PA (GUOX//) GUO X S.
 PA (HERR//) HERRMANN J L.
 PA (HALV//) HALVORSEN Y.
 PA (JIWU//) JI W.
 PA (KEKU//) KEKUDA R.
 PA (KHRA//) KHRAMTSOV N V.
 PA (LARO//) LAROCHELLE W J.
 PA (LEPL//) LEPLEY D M.
 PA (LILL//) LI L.
 PA (MACD//) MACDOUGALL J R.
 PA (MILL//) MILLER C E.
 PA (ORTT//) ORT T.
 PA (PADI//) PADIGARU M.
 PA (PATT//) PATTURAJAN M.
 PA (PENA//) PENA C E A.
 PA (PEYM//) PEYMAN J A.
 PA (RIEG//) RIEGER D K.
 PA (ROTH//) ROTHENBERG M E.
 PA (SHEN//) SHENOY S G.
 PA (SMIT//) SMITHSON G.
 PA (SPAD//) SPADERNA S K.
 PA (SPYT//) SPYTEK K A.
 PA (STON//) STONE D J.
 PA (TAUP//) TAUPIER R J.
 PA (VERN//) VERNET C A M.
 PA (VOSS//) VOSS E Z.
 PA (ZHON//) ZHONG M.
 XX
 PI Agee ML, Albrook JP, Anderson DW, Berghs C, Boldog FL,
 PI Burgess CE, Catterton E, Dipippo VA, Edinger SR, Eisen A;
 PI Ellerman K, Gangolli EA, Gerlach V, Gorman L, Rothberg BG, Guo XS;
 PI Herrmann JL, Halvorsen Y, Ji W, Kekuda R, Khrantsov NV,
 PI Larochele WJ, Lepley DM, Li L, Macdougall JR, Miller CE, Ort T;
 PI Padigaruru M, Patturajan M, Pena CE, Peyman JA, Rieger DK;
 PI Rothenberg ME, Shenoy SG, Smithson G, Spaderna SK, Spytek KA;
 PI Stone DJ, Taupier RJ, Vernet CAM, Voss EZ, Zhong M;
 XX
 DR WPI; 2004-268786/25.
 DR N-PSDB; ADO42300.
 XX
 PT New human NOVX polypeptides and nucleic acid molecules, useful for
 PT diagnosing, preventing or treating NOVX-associated disorder, e.g. cancer,
 PT atherosclerosis, diabetes, Alzheimer's disease, Parkinson's disease or
 PT scleroderma.
 XX
 PS Claim 1; SEQ ID NO 150; 610pp; English.

XX The invention relates to human NOVX polypeptides and the polynucleotides
 CC encoding them. The invention also relates to antibodies specific to the
 CC NOVX polypeptides. The polypeptides, polynucleotides and antibodies are
 CC useful for manufacturing a medicament for treating a syndrome associated
 CC with a human disease, such as a pathology associated with the NOVX
 CC polypeptide. The sequences are useful for diagnosing, treating or
 CC preventing a NOVX-associated disorder, e.g., cancer, atherosclerosis,
 CC diabetes, Alzheimer's disease, Parkinson's disease, graft-versus-host
 CC disease, scleroderma, hypertension, haemophilia, idiopathic
 CC thrombocytopenic purpura, immunodeficiencies, AIDS, dyslipidemia,
 CC obesity, Crohn's disease, bronchial asthma, anorexia, cancer-associated
 CC cachexia, multiple sclerosis or fertility. The nucleic acids may be used
 CC as hybridisation probes, in chromosome mapping, in tissue typing, in
 CC preventive medicine or in pharmacogenomics. This sequence represents a
 CC human NOVX polypeptide of the invention.
 XX
 SQ Sequence 734 AA;
 Query Match 97.1%; Score 2980; DB 8; Length 734;
 Best Local Similarity 78.2%; Pred. No. 9e-269;
 Matches 574; Conservative 0; Mismatches 0; Indels 160; Gaps 1;
 QY 1 MWGILLALAAPAPAVGAPALGAPRNSVLGLAQPGTKVPGSTPALHSSPAQPPAETANGTS 60
 DB 1 MWGILLALAAPAVGAPALGAPRNSVLGLAQPGTKVPGSTPALHSSPAQPPAETANGTS 60
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 DB 301 NYKAMRKLKMQVQECFNITRIYSIGKSYOGLKLYNMEMSDKPGHEHLPGEPEVRYVAGMH 360
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 DB 361 GNEALGRELLLLMQFLCHEFLRGNPRVTRLLEMRTHLLPSMNPDCGYEYAYHRGSELVG 420
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 DB 421 WAEGRWNNQSIDLNHNFPADLNTPLWEAQDQGVPHIVPNHHLPLPTTYTTLPNATVAPETR 480
 QY 481 AVIKMKRIPFVLSANLHGELVVSYPFD----- 509
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 QY 510 -----MVTASGYHSVTENCVTPEEGFPFCNFVLTPTKQRLRELLAAGAKVPP 560
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 QY 561 DLRRRLRLRGQXD 574
 DB 561 DLRRRLRLRGQXD 574

PS Claim 1; SEQ ID NO 154; 610pp; English.

CC The invention relates to human NOVX polypeptides and the polynucleotides

CC encoding them. The invention also relates to antibodies specific to the

CC NOVX polypeptides. The polypeptides, polynucleotides and antibodies are

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CC diabetes, Alzheimer's disease, Parkinson's disease, graft-versus-host

CC disease, scleroderma, hypertension, haemophilia, idiopathic

CC thrombocytopenic purpura, immunodeficiencies, AIDS, dyslipidemia,

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CC cachexia, multiple sclerosis or fertility. The nucleic acids may be used

CC as hybridisation probes, in chromosome mapping, in tissue typing, in

CC preventive medicine or in pharmacogenomics. This sequence represents a

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XX Sequence 734 AA;

SQ

Query Match 97.1%; Score 2980; DB 8; Length 734;

Best Local Similarity 78.2%; Pred. No. 9e-269;

Matches 574; Conservative 0; Mismatches 0; Indels 160; Gaps 1;

QY 1 MWGILLALAAPAVGALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS 60

DB 1 MWGILLALAAPAVGALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS 60

QY 61 EOHVRIIRIVIKKKVIMKKRKLTLTRPTPLVATGATVTPPTAGTLDPAEKQETCCPPLGL 120

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QY 241 NLPEPOVAFIRLLPOTLQGGAPCLRAETLACPVSDPNDLFLFAPASGSSDPLDQHH 300

DB 241 NLPEPOVAFIRLLPOTLQGGAPCLRAETLACPVSDPNDLFLFAPASGSSDPLDQHH 300

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QY 361 GNEALGRELLLLMQFLCHEFLRGNPRVTRLSEMRTHLLPSMNPDCGYEYAHRSSELVG 420

DB 361 GNEALGRELLLLMQFLCHEFLRGNPRVTRLSEMRTHLLPSMNPDCGYEYAHRSSELVG 420

QY 421 WAEGRWNNQSIDLNHNFADNLTPLEAQDQGVPHIVPNHHLLPLPTTYTTLPNATVAPETR 480

DB 421 WAEGRWNNQSIDLNHNFADNLTPLEAQDQGVPHIVPNHHLLPLPTTYTTLPNATVAPETR 480

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DB 481 AVIKWMKRIIPVLISANLHGELVVSYPFD----- 509

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DB 510 ----- 509

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DB 541 LAMQDTSRRPCHSQDSFVGHNIINGADWHTVPGSMNDFSYLHTNCPEVTVELSCDKFPHE 600

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QY 661 WRLLTPGDYVMTASAEVSHVTRNCRVTFEEGPPFCNFVLTQKRLRELLAAGAKVPP 720

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QY 561 DLRRRLRLRGQKD 574

Db 721 DLRRRLRLRGQKD 734

RESULT 12

ADO42307

ID ADO42307 standard; protein; 734 AA.

XX ADO42307;

AC ADO42307;

XX

DT 15-JUL-2004 (first entry)

XX Human NOVX polypeptide #78.

DE

XX Human; NOVX; cancer; atherosclerosis; diabetes; Alzheimer's disease;

XX Parkinson's disease; graft-versus-host disease; scleroderma;

XX hypertension; haemophilia; idiopathic thrombocytopenic purpura;

XX immunodeficiency; AIDS; dyslipidemia; obesity; Crohn's disease;

XX bronchial asthma; anorexia; cancer-associated cachexia;

XX multiple sclerosis; fertility.

OS Homo sapiens.

XX

XX US2004058338-A1.

XX 25-MAR-2004.

XX

PF 02-DEC-2002; 2002US-00307817.

XX

XX 03-DEC-2001; 2001US-0336881P.

PR 05-DEC-2001; 2001US-0336820P.

PR 07-DEC-2001; 2001US-0338285P.

PR 07-DEC-2001; 2001US-0338181P.

PR 10-DEC-2001; 2001US-0338989P.

PR 10-DEC-2001; 2001US-0339022P.

PR 11-DEC-2001; 2001US-0339314P.

PR 11-DEC-2001; 2001US-0339516P.

PR 11-DEC-2001; 2001US-0339517P.

PR 11-DEC-2001; 2001US-0339611P.

PR 12-DEC-2001; 2001US-0340981P.

PR 12-DEC-2001; 2001US-0341346P.

PR 14-DEC-2001; 2001US-0340390P.

PR 14-DEC-2001; 2001US-0340440P.

PR 14-DEC-2001; 2001US-0340565P.

PR 14-DEC-2001; 2001US-0340608P.

PR 14-DEC-2001; 2001US-0341144P.

PR 17-DEC-2001; 2001US-0341477P.

PR 17-DEC-2001; 2001US-0341540P.

PR 18-DEC-2001; 2001US-0341768P.

PR 20-DEC-2001; 2001US-0342592P.

PR 31-DEC-2001; 2001US-0344903P.

PR 01-FEB-2002; 2002US-0353286P.

PR 01-FEB-2002; 2002US-0353288P.

PR 26-FEB-2002; 2002US-0359599P.

PR 26-FEB-2002; 2002US-0359626P.

PR 26-FEB-2002; 2002US-0359671P.

PR 27-FEB-2002; 2002US-0359914P.

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PR 28-FEB-2002; 2002US-0360324P.

PR 28-FEB-2002; 2002US-0360964P.

PR 28-FEB-2002; 2002US-0361028P.

PR 28-FEB-2002; 2002US-0361256P.

PR 05-MAR-2002; 2002US-0361709P.

PR 05-MAR-2002; 2002US-0362230P.

PR 13-MAR-2002; 2002US-0364181P.

PR 13-MAR-2002; 2002US-0364238P.

PR 15-MAR-2002; 2002US-0364978P.

PR 15-MAR-2002; 2002US-0365025P.

PR 17-APR-2002; 2002US-0373288P.

PR 15-MAY-2002; 2002US-0380981P.

PR 16-MAY-2002; 2002US-0381004P.

PR 17-MAY-2002; 2002US-0381495P.

28-MAY-2002;	2002US-0383534P.
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28-MAY-2002;	2002US-0383744P.
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28-MAY-2002;	2002US-0383829P.
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28-MAY-2002;	2002US-0384024P.
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02-JUL-2002;	2002US-0393332P.
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06-AUG-2002;	2002US-0401315P.
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23-AUG-2002;	2002US-0405698P.
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PA	(ALSO/) ALSOBROOK J P.
PA	(ANDE/) ANDERSON D W.
PA	(BERG/) BERGHS C.
PA	(BOLD/) BOLDG F L.
PA	(BURG/) BURGESS C E.
PA	(CATT/) CATTERTON E.
PA	(DIPI/) DIPIPPO V A.
PA	(EDIN/) EDINGER S R.
PA	(EISE/) EISEN A.
PA	(ELLE/) ELLERMAN K.
PA	(GANG/) GANGOLLI E A.
PA	(GERL/) GERLACH V.
PA	(GORM/) GORMAN L.
PA	(ROTH/) ROTHBERG B G.
PA	(GUOX/) GUO X S.
PA	(HERR/) HERRMANN J L.
PA	(HALV/) HALVORSEN Y.
PA	(JIWV/) JI W.
PA	(KEKU/) KEKUDA R.
PA	(KHRA/) KHRAMTSOV N V.
PA	(LARO/) LAROCHELLE W J.
PA	(LEPL/) LEPPLEY D M.
PA	(LILL/) LI L.
PA	(MACD/) MACDOUGALL J R.
PA	(MILL/) MILLER C E.
PA	(ORTT/) ORT T.
PA	(PADI/) PADIGARU M.
PA	(PATT/) PATTURAJAN M.
PA	(PENA/) PENA C E A.
PA	(PEYM/) PEYMAN J A.
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PA	(ROTH/) ROTHENBERG M E.
PA	(SHEN/) SHENOY S G.
PA	(SMIT/) SMITHSON G.
PA	(SPAD/) SPADERNA K A.
PA	(SPYT/) SPYTEK K A.
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PA	(VERN/) VERNET C A M.
PA	(VOSS/) VOSS E Z.
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PI	Ellerman K, Gangolli EA, Gerlach V, Gorman L, Rothberg BG,
PI	Herrmann J, Halvorsen Y, Ji W, Kekuda R, Khrantsov NV;
PI	Larochelle WJ, Leppley DM, Li L, Macdougall JR, Miller CE, Ort T;
PI	Padigar M, Patturajan M, Pena CE, Peyman JA, Rieger DK;
PI	Rothenberg ME, Shenoj SG, Smithson G, Spaderna SK, Spytek KA;
PI	Stone DJ, Taupier RJ, Vernet CAM, Voss EZ, Zhong M;
XX	
DR	WPI: 2004-268786/25.
DR	N-PSDB; ADO42306.
XX	
XX	New human NOVX polypeptides and nucleic acid molecules, useful for
PPT	diagnosing, preventing or treating NOVX-associated disorder, e.g., cancer,
PPT	atherosclerosis, diabetes, Alzheimer's disease, Parkinson's disease or
PPT	scleroderma.

PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000WO-US034956.
XX
PA (GETH) GENENTECH INC.
XX
XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski FU, Gurney AL;
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
XX
XX WPI, 2001-602746/68.
DR N-FSDb; AAS46153.
DR
XX
XX Novel nucleic acids encoding PRO polypeptides, used to diagnose the
PT presence of tumors, such as prostate and breast tumors, in mammals and to
PT screen for modulators of the compounds.
XX
XX Claim 11; Fig 458; 774pp; English.
XX
XX Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.
XX The PRO polypeptides and their associated nucleic acids can be used to
CC detect the presence of a tumor in a mammal by comparing the level of
CC expression of a PRO polypeptide in a test sample of cells from the animal
CC and a control sample of normal cells, whereby a higher level of
CC expression in the test sample indicates the presence of a tumor in the
CC mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats
CC and rabbits but are preferably human. The polypeptides can be used to
CC stimulate tumour necrosis factor (TNF) alpha release from human blood,
CC when contacted with it. A specific polypeptide can be used to stimulate
CC the proliferation or differentiation of chondrocyte cells. The PRO
CC proteins can be used to determine the presence of tumours and also
CC susceptibility to tumour development, particularly adrenal, lung, colon,
CC breast, prostate, rectal, cervical, or liver tumours, in mammalian
CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
CC can be used for genetic analysis of individuals with genetic disorders
XX
SQ Sequence 734 AA;

Query Match 96.9%; Score 2975; DB 4; Length 734;
Best Local Similarity 78.1%; Pred. No. 2.6e-268;
Matches 573; Conservative 0; Mismatches 1; Indels 160; Gaps 1;

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Db 1 MWGLLLAALAPAPAVGAPALGAPRNSVLGLAQGTTKVPGSTPALHSSPAQPPAETANGTS 60

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QY 361 GNEALGRELLLLMQFLCHEFLGRNPRVTRLLSEMRIHLPSMNPDCGYEYAYHRGSELVG 420
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Db 661 WRLLTPGDYMTVMTASAEGYHSVTRNCRVTFEEGPPPCNFVLTCTPKQRLRELLAAGAKVPP 720
QY 561 DLRRRLERLRGQKD 574
Db 721 DLRRRLERLRGQKD 734

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OM protein - protein search, using sw model

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	3070	100.0	574	15	Sequence 6, Appli
3	3070	100.0	574	15	Sequence 170, App
4	2980	97.1	734	10	Sequence 152, App
5	2980	97.1	734	10	Sequence 2, Appli
6	2980	97.1	734	14	Sequence 65, Appl
7	2980	97.1	734	15	Sequence 168, App
8	2980	97.1	734	15	Sequence 174, App
9	2980	97.1	734	15	Sequence 150, App
10	2980	97.1	734	15	Sequence 154, App
11	2976	96.9	734	15	Sequence 156, App
12	2976	96.9	734	14	Sequence 38, Appl
13	2976	96.9	734	15	Sequence 38, Appl

14	2976	96.9	734	16	US-10-689-832-38	Sequence 38, Appl
15	2975	96.9	734	13	US-10-052-586-458	Sequence 458, App
16	2975	96.9	734	14	US-10-174-590-458	Sequence 458, App
17	2975	96.9	734	14	US-10-176-758-458	Sequence 458, App
18	2975	96.9	734	14	US-10-175-737-458	Sequence 458, App
19	2975	96.9	734	14	US-10-174-581-458	Sequence 458, App
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21	2975	96.9	734	14	US-10-176-749-458	Sequence 458, App
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25	2975	96.9	734	14	US-10-175-738-458	Sequence 458, App
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27	2975	96.9	734	14	US-10-176-482-458	Sequence 458, App
28	2975	96.9	734	14	US-10-176-757-458	Sequence 458, App
29	2975	96.9	734	14	US-10-176-913-458	Sequence 458, App
30	2975	96.9	734	14	US-10-180-552-458	Sequence 458, App
31	2975	96.9	734	14	US-10-180-557-458	Sequence 458, App
32	2975	96.9	734	14	US-10-173-700-458	Sequence 458, App
33	2975	96.9	734	14	US-10-174-572-458	Sequence 458, App
34	2975	96.9	734	14	US-10-174-579-458	Sequence 458, App
35	2975	96.9	734	14	US-10-174-582-458	Sequence 458, App
36	2975	96.9	734	14	US-10-174-588-458	Sequence 458, App
37	2975	96.9	734	14	US-10-175-739-458	Sequence 458, App
38	2975	96.9	734	14	US-10-175-740-458	Sequence 458, App
39	2975	96.9	734	14	US-10-175-743-458	Sequence 458, App
40	2975	96.9	734	14	US-10-176-488-458	Sequence 458, App
41	2975	96.9	734	14	US-10-176-492-458	Sequence 458, App
42	2975	96.9	734	14	US-10-176-747-458	Sequence 458, App
43	2975	96.9	734	14	US-10-176-750-458	Sequence 458, App
44	2975	96.9	734	14	US-10-176-985-458	Sequence 458, App
45	2975	96.9	734	14	US-10-176-987-458	Sequence 458, App

ALIGNMENTS

RESULT 1

US-09-996-015-6
; Sequence 6, Application US/09996015
; Publication No. US20030032166A1
; GENERAL INFORMATION:
; APPLICANT: Quinn, Kerry E.
; APPLICANT: Li, Li
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Leite, Marlo W.
; TITLE OF INVENTION: Aortic Carboxypeptidase-Like Proteins and Nucleic Acids
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 15966-581 CIP
; CURRENT APPLICATION NUMBER: US/09/996,015
; CURRENT FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: 09/641,741
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: 60/159,613
; PRIOR FILING DATE: 1999-10-14
; PRIOR APPLICATION NUMBER: 60/175,534
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 60/224,086
; PRIOR FILING DATE: 2000-08-09
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-015-6

Query Match 100.0%; Score 3070; DB 10; Length 574;
Best Local Similarity 100.0%; Pred. No. 2e-259;
Matches 574; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MWGLLLAALAFAPAVGPAFGPNVSLGLAQPGTKVPGSTPALHSSPAQPPAETANGTS 60

Db	1	MWGLLLALAAFAVAGPALGNRSVLGLAQPGTTKVPGSTPALRHSSPAQPAETANGTS	1
Qy	61	EOHVRIRVIKKKKVIMKKRKKLILTRPTPLVTAGPLVPTTPAGTILDPAEKQETGCPPLGL	1
Db	61	EOHVRIRVIKKKKVIMKKRKKLILTRPTPLVTAGPLVPTTPAGTILDPAEKQETGCPPLGL	1
Qy	121	ESLRVSDSRLEASSSSQSGFLGPHRGRLINTQSGLEPGDLYDGAWCAEBQADPWFQVDAGH	1
Db	121	ESLRVSDSRLEASSSSQSGFLGPHRGRLINTQSGLEPGDLYDGAWCAEBQADPWFQVDAGH	1
Qy	181	PTPFSGVITQGRNSVRYDWTYSYKVORNSDRTWGSRNHSSGMDAVFPANSPETPVL	2
Db	181	PTPFSGVITQGRNSVRYDWTYSYKVORNSDRTWGSRNHSSGMDAVFPANSPETPVL	2
Qy	241	NLLPEQVAFRILLPOTWLQGCAPCLRAEILLACVSPDNILFLEAPASSGSDPLDPQHH	3
Db	241	NLLPEQVAFRILLPOTWLQGCAPCLRAEILLACVSPDNILFLEAPASSGSDPLDPQHH	3
Qy	301	NYKAMKLMKQVQBQCPNTRIYSIGKSVQGLKLYWEMSDKPGHEHLPBEVRYAGMH	3
Db	301	NYKAMKLMKQVQBQCPNTRIYSIGKSVQGLKLYWEMSDKPGHEHLPBEVRYAGMH	3
Qy	361	GNELGRELIILLMOPFLCHEFLRGHPNVRTLLSEMRHLLPSMNPDCGYEAYHRGSELVG	4
Db	361	GNELGRELIILLMOPFLCHEFLRGHPNVRTLLSEMRHLLPSMNPDCGYEAYHRGSELVG	4
Qy	421	WAEGRWNNSIIDLINHFADNLPLWEAQDDGKVPHIVENHHLPLPTYTYTLPNATVAPEIR	4
Db	421	WAEGRWNNSIIDLINHFADNLPLWEAQDDGKVPHIVENHHLPLPTYTYTLPNATVAPEIR	4
Qy	481	AVIKWMKRIPFVLISANLHGGELVVSYPDFDMVTASAEGVHSVTRNCRVTFEEGPPPCNFVL	5
Db	481	AVIKWMKRIPFVLISANLHGGELVVSYPDFDMVTASAEGVHSVTRNCRVTFEEGPPPCNFVL	5
Qy	541	TKTPQRLRELLAAGAKVPPDPLRRRLERLRQKD	574
Db	541	TKTPQRLRELLAAGAKVPPDPLRRRLERLRQKD	574

```

RESULT 2
US-10-287-190-170
; Sequence 170, Application US/10287190
; Publication No. US2004003230A1
; GENERAL INFORMATION:
;
; APPLICANT: Alsbrook II, John P. et al
;
; TITLE OF INVENTION: 21402-780B, THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS OF USE
;
; FILE REFERENCE: 21402-780B
;
; CURRENT APPLICATION NUMBER: US/10/287,190
;
; CURRENT FILING DATE: 2003-04-02
;
; PRIOR APPLICATION NUMBER: 09/7996,015
;
; PRIOR FILING DATE: 2001-11-26/38626
;
; PRIOR APPLICATION NUMBER: 60/338626
;
; PRIOR FILING DATE: 2001-11-05/373806
;
; PRIOR APPLICATION NUMBER: 60/373806
;
; PRIOR FILING DATE: 2002-04-19
;
; PRIOR APPLICATION NUMBER: 60/338196
;
; PRIOR FILING DATE: 2001-12-03
;
; PRIOR APPLICATION NUMBER: 60/333912
;
; PRIOR FILING DATE: 2001-11-28
;
; PRIOR APPLICATION NUMBER: 60/381043
;
; PRIOR FILING DATE: 2002-05-16
;
; PRIOR APPLICATION NUMBER: 60/401593
;
; PRIOR FILING DATE: 2002-08-07
;
; PRIOR APPLICATION NUMBER: 60/334300
;
; NUMBER OF SEQ ID NOS: 194
;
; SOFTWARE: Curasequest version 0.1
;
; SEQ ID NO 170
;
; LENGTH: 574
;
; TYPE: PRT
;
; ORIGIN: Homo sapiens
US-10-287-190-170

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Query Match	100.0%	Score	3070;	DB	15;	Length	574;
Best Local Similarity	100.0%	Pred.	No. 2e-259;				
Matches	574;	Conservative	0;	Mismatches	0;	Indels	0;
QY	1	MWGLLLAALAAPAVAGVPALGAPRNSVLGLAQGGTTTKVFGSTPALHSSPAQPAETANGTS	60				
DB	1	MWGLLLAALAAPAVAGVPALGAPRNSVLGLAQGGTTTKVFGSTPALHSSPAQPAETANGTS	60				
QY	61	EOHVRIRVKKKKVIMKKRKKILTLRPTPLVTVAGPLVTPTPAGTILDPAEKQSTGCPPLGL	120				
DB	61	EOHVRIRVKKKKVIMKKRKKILTLRPTPLVTVAGPLVTPTPAGTILDPAEKQSTGCPPLGL	120				
QY	121	ESLRVSDSRLEASSSQSFCGLGPHRGLNIQSGLEDGLYDGAWCAEEOADPWFQVDAGH	180				
DB	121	ESLRVSDSRLEASSSQSFCGLGPHRGLNIQSGLEDGLYDGAWCAEEOADPWFQVDAGH	180				
QY	181	PTRFSGVITQGRNSVVRVYDWTYSYKQFSNDPNSRTVMGSRNHSNGMDVFPANSDPETPVL	240				
DB	181	PTRFSGVITQGRNSVVRVYDWTYSYKQFSNDPNSRTVMGSRNHSNGMDVFPANSDPETPVL	240				
QY	241	NLLPSPQVARTIRILLPQTWLOGGAPCLRAEILACVPSPDPNDLFLPAPAGSGSDPLDFQHH	300				
DB	241	NLLPSPQVARTIRILLPQTWLOGGAPCLRAEILACVPSPDPNDLFLPAPAGSGSDPLDFQHH	300				
QY	301	NYKAMRKLIMKQVQEQCPNITRIYSIGKSYQGLKYVMEMSDKPGHEHLCGEFVRYVAGMH	360				
DB	301	NYKAMRKLIMKQVQEQCPNITRIYSIGKSYQGLKYVMEMSDKPGHEHLCGEFVRYVAGMH	360				
QY	361	GNEALGRELLILLMOFLCHEFLRGNPVRTLLSEMRHLPLSMNPDGVEIAYHRGSELVG	420				
DB	361	GNEALGRELLILLMOFLCHEFLRGNPVRTLLSEMRHLPLSMNPDGVEIAYHRGSELVG	420				
QY	421	WAEGRWNQSIDLNNFNADNLPLWEAQDQGVPHIVGNHHLPLPTYTITPLNATVAETPR	480				
DB	421	WAEGRWNQSIDLNNFNADNLPLWEAQDQGVPHIVGNHHLPLPTYTITPLNATVAETPR	480				
QY	481	AVIKWMKRIEPLVLSANLHGELVYSYFDMVTASAGYHSVTRNCRVTFBEGPPPCNFVL	540				
DB	481	AVIKWMKRIEPLVLSANLHGELVYSYFDMVTASAGYHSVTRNCRVTFBEGPPPCNFVL	540				
QY	541	TKTPKQRLRELLAAGAKVPPDLRRRLRLRGQXD	574				
DB	541	TKTPKQRLRELLAAGAKVPPDLRRRLRLRGQXD	574				
RESULT 3							
US-10-307-817-152							
; Sequence 152, Application US/10307817							
; Publication No. US20040058338A1							
; GENERAL INFORMATION:							
; APPLICANT: Agee et al.							
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME							
; FILE REFERENCE: 21402-502C							
; CURRENT APPLICATION NUMBER: US/10/307,817							
; CURRENT FILING DATE: 2002-12-02							
; NUMBER OF SEQ ID NOS: 682							
; SOFTWARE: CuroSeqList version 0.1							
; SEQ ID NO 152							
; LENGTH: 574							
; TYPE: PRT							
; ORGANISM: Homo sapiens							
US-10-307-817-152							

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Query Match      100.0%; Score 3070; DB 15; Length 574;
Best Local Similarity 100.0%; Pred. No. 2e-359;
Matches 574; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLLLLAAPAPAVGPFALGAPRNSVLGLQAQGTGTTKVGSTPALHSSPAQPPAETANGTS 60
   |||||
Db 1 MGLLLLAAPAPAVGPFALGAPRNSVLGLQAQGTGTTKVGSTPALHSSPAQPPAETANGTS 60
   |||||

QY 61 ECHVRIRVTKKKVIMKKRKKLTLRTPETPLVTAGPLVTPTAGTLDLPASKQGTGCPPLGL 120

```


Db 61 EQHVRIRVIKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPAGTLDPAEKQETGCPPLGL 120
QY 121 ESLRVSRLAEASSQSFGFLGPHRGRNLNIOGLEDGLYDGAWCAEQDADPWFQVDAGH 180
Db 121 ESLRVSRLAEASSQSFGFLGPHRGRNLNIOGLEDGLYDGAWCAEQDADPWFQVDAGH 180
QY 181 PTFSGVITQGRNSVMRYDWTYSYKQVFSNDSRTWGSRNHSSGMDAVFPANSDPETPVL 240
Db 181 PTFSGVITQGRNSVMRYDWTYSYKQVFSNDSRTWGSRNHSSGMDAVFPANSDPETPVL 240
QY 241 NLLPEPOVARFIRLLPQTLQGGAPCLRAEILACPVSDPNDLFLAEPASGSSDPLDFQHH 300
Db 241 NLLPEPOVARFIRLLPQTLQGGAPCLRAEILACPVSDPNDLFLAEPASGSSDPLDFQHH 300
QY 301 NYKAMRKLKMQVOEQCPNITRIYSIGKSYOGLKLYNMESDKPGEHELGEPEVRYVAGMH 360
Db 301 NYKAMRKLKMQVOEQCPNITRIYSIGKSYOGLKLYNMESDKPGEHELGEPEVRYVAGMH 360
QY 361 GNEALGRELLLLMQFLCHEFLRGPNRVTLLSEMRIHLLPSMNPDCGYEYAIHRGSELVG 420
Db 361 GNEALGRELLLLMQFLCHEFLRGPNRVTLLSEMRIHLLPSMNPDCGYEYAIHRGSELVG 420
QY 421 WBSGRWNNQSIDLNHNFADLNTPLWEAQDDGKVPHIIPNHHLLPLPTYYTLPNATVAPETR 480
Db 421 WBSGRWNNQSIDLNHNFADLNTPLWEAQDDGKVPHIIPNHHLLPLPTYYTLPNATVAPETR 480
QY 481 AVIKWMKRIPFVLSANLHGGLVVSYPFDMVTASAGYHSVTRNCRVTFEEGPPPCNCFVL 540
Db 481 AVIKWMKRIPFVLSANLHGGLVVSYPFDMVTASAGYHSVTRNCRVTFEEGPPPCNCFVL 540
QY 541 TKTPKQRLRELLAAGAKVPPDLRRRLRLRGQKD 574
Db 541 TKTPKQRLRELLAAGAKVPPDLRRRLRLRGQKD 574

RESULT 4
US-09-996-015-2
; Sequence 2, Application US/09996015
; Publication No. US20030032166A1
; GENERAL INFORMATION:
; APPLICANT: Quinn, Kerry E.
; APPLICANT: Li, Li
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Leite, Marlo W.
; TITLE OF INVENTION: Aortic Carboxypeptidase-Like Proteins and Nucleic Acids
; FILE OF INVENTION: Encoding Same
; FILE REFERENCE: 15966-581 CIP
; CURRENT FILING DATE: 2001-11-28
; PRIOR FILING DATE: 2001-11-28
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: 60/159,613
; PRIOR FILING DATE: 1999-10-14
; PRIOR APPLICATION NUMBER: 60/175,534
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 60/224,086
; PRIOR FILING DATE: 2000-08-09
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 734
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-015-2
Query Match 97.1%; Score 2980; DB 10; Length 734;
Best Local Similarity 78.2%; Pred. No. 2.2e-251;
Matches 574; Conservative 0; Mismatches 0; Indels 160; Gaps 1;
QY 1 MWGLLLAALAFAPAVGALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS 60
|||||

Db 1 MWGLLLAALAFAPAVGALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS 60
QY 61 EQHVRIRVIKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPAGTLDPAEKQETGCPPLGL 120
Db 61 EQHVRIRVIKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPAGTLDPAEKQETGCPPLGL 120
QY 121 ESLRVSRLAEASSQSFGFLGPHRGRNLNIOGLEDGLYDGAWCAEQDADPWFQVDAGH 180
Db 121 ESLRVSRLAEASSQSFGFLGPHRGRNLNIOGLEDGLYDGAWCAEQDADPWFQVDAGH 180
QY 181 PTFSGVITQGRNSVMRYDWTYSYKQVFSNDSRTWGSRNHSSGMDAVFPANSDPETPVL 240
Db 181 PTFSGVITQGRNSVMRYDWTYSYKQVFSNDSRTWGSRNHSSGMDAVFPANSDPETPVL 240
QY 241 NLLPEPOVARFIRLLPQTLQGGAPCLRAEILACPVSDPNDLFLAEPASGSSDPLDFQHH 300
Db 241 NLLPEPOVARFIRLLPQTLQGGAPCLRAEILACPVSDPNDLFLAEPASGSSDPLDFQHH 300
QY 301 NYKAMRKLKMQVOEQCPNITRIYSIGKSYOGLKLYNMESDKPGEHELGEPEVRYVAGMH 360
Db 301 NYKAMRKLKMQVOEQCPNITRIYSIGKSYOGLKLYNMESDKPGEHELGEPEVRYVAGMH 360
QY 361 GNEALGRELLLLMQFLCHEFLRGPNRVTLLSEMRIHLLPSMNPDCGYEYAIHRGSELVG 420
Db 361 GNEALGRELLLLMQFLCHEFLRGPNRVTLLSEMRIHLLPSMNPDCGYEYAIHRGSELVG 420
QY 421 WBSGRWNNQSIDLNHNFADLNTPLWEAQDDGKVPHIIPNHHLLPLPTYYTLPNATVAPETR 480
Db 421 WBSGRWNNQSIDLNHNFADLNTPLWEAQDDGKVPHIIPNHHLLPLPTYYTLPNATVAPETR 480
QY 481 AVIKWMKRIPFVLSANLHGGLVVSYPFDMVTASAGYHSVTRNCRVTFEEGPPPCNCFVL 540
Db 481 AVIKWMKRIPFVLSANLHGGLVVSYPFDMVTASAGYHSVTRNCRVTFEEGPPPCNCFVL 540
QY 541 TKTPKQRLRELLAAGAKVPPDLRRRLRLRGQKD 574
Db 541 TKTPKQRLRELLAAGAKVPPDLRRRLRLRGQKD 574
RESULT 5
US-10-239-663-65
; Sequence 65, Application US/10239663
; Publication No. US20030139572A1
; GENERAL INFORMATION:
; APPLICANT: Agarwal, Pankaj
; APPLICANT: Murdoch, Paul R.
; APPLICANT: Rizvi, Safia, K.
; APPLICANT: Smith, Randall, F.
; APPLICANT: Xiang, Zhaoying
; APPLICANT: Kabnick, Karen
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50018
; CURRENT APPLICATION NUMBER: US/10/239,663
; CURRENT FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: PCT/US01/09226
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 60/192,158
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/192,668
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: 60/200,166

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/ PRIOR FILING DATE: 2000-04-27
/ NUMBER OF SEQ ID NOS: 66
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 65
/ LENGTH: 734
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-239-663-65

Query Match      97.1%; Score 2980; DB 14; Length 734;
Best Local Similarity 78.2%; Pred. No. 2.2e-251;
Matches 574; Conservative 0; Mismatches 0; Indels 160; Gaps 1;

QY 1 MWGLLALAAPAPAVGALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS 61
Db 1 MWGLLALAAPAPAVGALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS 61
QY 61 EOHVRIRIVIKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTTPTAGTLDPAEKQETCCPLGL 10
Db 61 EOHVRIRIVIKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTTPTAGTLDPAEKQETCCPLGL 10
QY 121 ESLRVSRLSEASSQSFGGLGPHRGRLNIQSGLEDGLYDGCACAEQDADPWFQVDAGH 10
Db 121 ESLRVSRLSEASSQSFGGLGPHRGRLNIQSGLEDGLYDGCACAEQDADPWFQVDAGH 10
QY 181 PTRFSGVITQGRNSVWRYDWVTSYKVQFSNDSRTWMSRHHSSGMDAVFPANSDPETPVL 20
Db 181 PTRFSGVITQGRNSVWRYDWVTSYKVQFSNDSRTWMSRHHSSGMDAVFPANSDPETPVL 20
QY 241 NLLPEQVAFIRLLPOTLQGGAPCLRAEILACPVSDPNDLFLFAPASGSSDPLDFQHH 30
Db 241 NLLPEQVAFIRLLPOTLQGGAPCLRAEILACPVSDPNDLFLFAPASGSSDPLDFQHH 30
QY 301 NYKAMRLMKQVQEQCPNITRIYSIGKSYQGLKLYVMEMSDKPGHEHGEPEVRYVAGMH 30
Db 301 NYKAMRLMKQVQEQCPNITRIYSIGKSYQGLKLYVMEMSDKPGHEHGEPEVRYVAGMH 30
QY 361 GNEALGRELLLLMQFLCHEFLRGNPRVTRLLSEMRTHLLPSMNPDCGYEYAIHRGSELVG 40
Db 361 GNEALGRELLLLMQFLCHEFLRGNPRVTRLLSEMRTHLLPSMNPDCGYEYAIHRGSELVG 40
QY 421 WAEGRWNNQSIDLNHNFPADLNTPLWEAQDDGKVPHTVPNHHLPLPTTYTLPNATVAPETR 40
Db 421 WAEGRWNNQSIDLNHNFPADLNTPLWEAQDDGKVPHTVPNHHLPLPTTYTLPNATVAPETR 40
QY 481 AVIKWKKRIIPFVLSANLHGGLVVSYPFD-----509
Db 481 AVIKWKKRIIPFVLSANLHGGLVVSYPFD-----509
QY 510 -----509
Db 541 LAMQDTSRRPCHSQDFSVHGNINGADWHTVPGSMNDFSYLHNCFEVTVLSCDKFPHE 600
QY 510 -----509

RESULT 6
US-10-287-190-168
/ Sequence 168, Application US10287190
/ Publication No. US20040038230A1
/ GENERAL INFORMATION:
/ APPLICANT: Alisobrook II, John P. et al.
/ TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
```

```
/ FILE REFERENCE: 21402-780B
/ CURRENT APPLICATION NUMBER: US/10/287,190
/ CURRENT FILING DATE: 2003-04-02
/ PRIOR APPLICATION NUMBER: 09/996,015
/ PRIOR FILING DATE: 2001-11-28
/ PRIOR APPLICATION NUMBER: 60/338626
/ PRIOR FILING DATE: 2001-11-05
/ PRIOR APPLICATION NUMBER: 60/373806
/ PRIOR FILING DATE: 2002-04-19
/ PRIOR APPLICATION NUMBER: 60/338196
/ PRIOR FILING DATE: 2001-12-03
/ PRIOR APPLICATION NUMBER: 60/333912
/ PRIOR FILING DATE: 2001-11-28
/ PRIOR APPLICATION NUMBER: 60/381043
/ PRIOR FILING DATE: 2002-05-16
/ PRIOR APPLICATION NUMBER: 60/401593
/ PRIOR FILING DATE: 2002-08-07
/ PRIOR APPLICATION NUMBER: 60/334300
/ PRIOR FILING DATE: 2001-11-29
/ NUMBER OF SEQ ID NOS: 194
/ SOFTWARE: CuraSeqList version 0.1
/ SEQ ID NO 168
/ LENGTH: 734
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-287-190-168

Query Match      97.1%; Score 2980; DB 15; Length 734;
Best Local Similarity 78.2%; Pred. No. 2.2e-251;
Matches 574; Conservative 0; Mismatches 0; Indels 160; Gaps 1;

QY 1 MWGLLALAAPAPAVGALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS 60
Db 1 MWGLLALAAPAPAVGALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS 60
QY 61 EOHVRIRIVIKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTTPTAGTLDPAEKQETCCPLGL 120
Db 61 EOHVRIRIVIKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTTPTAGTLDPAEKQETCCPLGL 120
QY 121 ESLRVSRLSEASSQSFGGLGPHRGRLNIQSGLEDGLYDGCACAEQDADPWFQVDAGH 180
Db 121 ESLRVSRLSEASSQSFGGLGPHRGRLNIQSGLEDGLYDGCACAEQDADPWFQVDAGH 180
QY 181 PTRFSGVITQGRNSVWRYDWVTSYKVQFSNDSRTWMSRHHSSGMDAVFPANSDPETPVL 240
Db 181 PTRFSGVITQGRNSVWRYDWVTSYKVQFSNDSRTWMSRHHSSGMDAVFPANSDPETPVL 240
QY 241 NLLPEQVAFIRLLPOTLQGGAPCLRAEILACPVSDPNDLFLFAPASGSSDPLDFQHH 300
Db 241 NLLPEQVAFIRLLPOTLQGGAPCLRAEILACPVSDPNDLFLFAPASGSSDPLDFQHH 300
QY 301 NYKAMRLMKQVQEQCPNITRIYSIGKSYQGLKLYVMEMSDKPGHEHGEPEVRYVAGMH 360
Db 301 NYKAMRLMKQVQEQCPNITRIYSIGKSYQGLKLYVMEMSDKPGHEHGEPEVRYVAGMH 360
QY 361 GNEALGRELLLLMQFLCHEFLRGNPRVTRLLSEMRTHLLPSMNPDCGYEYAIHRGSELVG 420
Db 361 GNEALGRELLLLMQFLCHEFLRGNPRVTRLLSEMRTHLLPSMNPDCGYEYAIHRGSELVG 420
QY 421 WAEGRWNNQSIDLNHNFPADLNTPLWEAQDDGKVPHTVPNHHLPLPTTYTLPNATVAPETR 480
Db 421 WAEGRWNNQSIDLNHNFPADLNTPLWEAQDDGKVPHTVPNHHLPLPTTYTLPNATVAPETR 480
QY 481 AVIKWKKRIIPFVLSANLHGGLVVSYPFD-----509
Db 481 AVIKWKKRIIPFVLSANLHGGLVVSYPFD-----509
QY 510 -----509
Db 541 LAMQDTSRRPCHSQDFSVHGNINGADWHTVPGSMNDFSYLHNCFEVTVLSCDKFPHE 600
QY 510 -----509
```

Db 601 NELPQEWNNKDALTYLEQVRMGIAGVVRDKDTLGIADAVIAVDGINHDVTAMGGDY 660
Qy 510 -----MVTASAEYHSVTRNCRVTFEEGPPPCNFVLTCTPKQRLRELLAAGAKVPP 560
Db 661 WRLLTGCDYMWIASAEYHSVTRNCRVTFEEGPPPCNFVLTCTPKQRLRELLAAGAKVPP 720
Qy 561 DLRRRLRLRGQKD 574
Db 721 DLRRRLRLRGQKD 734
RESULT 7
US-10-287-190-174
; Sequence 174, Application US/10287190
; Publication No. US20040038230A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John P. et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-780B
; CURRENT APPLICATION NUMBER: US/10/287,190
; PRIOR FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 09/996,015
; PRIOR FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: 60/338626
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 60/373806
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/338196
; PRIOR FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/333912
; PRIOR FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: 60/381043
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/401593
; PRIOR FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: 60/334300
; PRIOR FILING DATE: 2001-11-29
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 174
; TYPE: PRT
; LENGTH: 734
; ORGANISM: Homo sapiens
US-10-287-190-174
Query Match 97.1%; Score 2980; DB 15; Length 734;
Best Local Similarity 78.2%; Pred. No. 2.2e-251;
Matches 574; Conservative 0; Mismatches 0; Indels 160; Gaps 1;
Qy 1 MMGLLLAALAAFAVAPGALGAPNSVLGLAQPGCTTKVPGSTPALHSSPAQPPAETANGTS 60
Db 1 MMGLLLAALAAFAVAPGALGAPNSVLGLAQPGCTTKVPGSTPALHSSPAQPPAETANGTS 60
Qy 61 EQHVRIRVTKKKKVIKKKVKILTKRTPPLVTAGPLVTPPTAGTLPDAEKQETGCPPLGL 120
Db 61 EQHVRIRVTKKKKVIKKKVKILTKRTPPLVTAGPLVTPPTAGTLPDAEKQETGCPPLGL 120
Qy 121 ESLRVSDSRLEASSSSQSGFLGPHRGRLNITQSGLEDGLYDGAWCAEQDADPMFQVDAGH 180
Db 121 ESLRVSDSRLEASSSSQSGFLGPHRGRLNITQSGLEDGLYDGAWCAEQDADPMFQVDAGH 180
Qy 181 PTFRFSGVITQGRNSVMRYDWTYSYKQFNSDRTWGSRNHSSGMDAVFPANSDPTPTVL 240
Db 181 PTFRFSGVITQGRNSVMRYDWTYSYKQFNSDRTWGSRNHSSGMDAVFPANSDPTPTVL 240
Qy 241 NLLPEQVARFIRLLPOTWLGQCAPCLRAEILACPVSDPNDLFLFAPASGSSDPLDFQHH 300
Db 241 NLLPEQVARFIRLLPOTWLGQCAPCLRAEILACPVSDPNDLFLFAPASGSSDPLDFQHH 300
Qy 301 NYKAMEKLMKQVQEQCPNITRIYSICKSYQGLKLYNMEMSDKPEHELGEPEVRYVAGMH 360
Db 301 NYKAMEKLMKQVQEQCPNITRIYSICKSYQGLKLYNMEMSDKPEHELGEPEVRYVAGMH 360

Qy 361 GNEALGRELLELLLMQFLCHEFLRGNPRVTRLLESMRIHLLPSMNPDCGYEIAYHRGSELVG 420
Db 361 GNEALGRELLELLLMQFLCHEFLRGNPRVTRLLESMRIHLLPSMNPDCGYEIAYHRGSELVG 420
Qy 421 WAEGRWNNQSIDLNNFADLNTPLWEAQDDCKVPHIVPNHHLPLPTYYTTPNATVAPETR 480
Db 421 WAEGRWNNQSIDLNNFADLNTPLWEAQDDCKVPHIVPNHHLPLPTYYTTPNATVAPETR 480
Qy 481 AVIKMMKRIPFVLSANLHGELVVSYPFD----- 509
Db 481 AVIKMMKRIPFVLSANLHGELVVSYPFD----- 509
Qy 510 ----- 509
Db 541 LAMQDTSRRPCHSQDSVHGNIINGADWHTVPGSMNDFSYLHTNCFEVTVELSCDKPPHE 600
Qy 510 ----- 509
Db 601 NELPQEWNNKDALTYLEQVRMGIAGVVRDKDTLGIADAVIAVDGINHDVTAMGGDY 660
Qy 510 -----MVTASAEYHSVTRNCRVTFEEGPPPCNFVLTCTPKQRLRELLAAGAKVPP 560
Db 661 WRLLTGCDYMWIASAEYHSVTRNCRVTFEEGPPPCNFVLTCTPKQRLRELLAAGAKVPP 720
Qy 561 DLRRRLRLRGQKD 574
Db 721 DLRRRLRLRGQKD 734
RESULT 8
US-10-307-817-150
; Sequence 150, Application US/10307817
; Publication No. US20040058338A1
; GENERAL INFORMATION:
; APPLICANT: Agee et al.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-502C
; CURRENT APPLICATION NUMBER: US/10/307,817
; CURRENT FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 682
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 150
; TYPE: PRT
; LENGTH: 734
; ORGANISM: Homo sapiens
US-10-307-817-150
Query Match 97.1%; Score 2980; DB 15; Length 734;
Best Local Similarity 78.2%; Pred. No. 2.2e-251;
Matches 574; Conservative 0; Mismatches 0; Indels 160; Gaps 1;
Qy 1 MMGLLLAALAAFAVAPGALGAPNSVLGLAQPGCTTKVPGSTPALHSSPAQPPAETANGTS 60
Db 1 MMGLLLAALAAFAVAPGALGAPNSVLGLAQPGCTTKVPGSTPALHSSPAQPPAETANGTS 60
Qy 61 EQHVRIRVTKKKKVIKKKVKILTKRTPPLVTAGPLVTPPTAGTLPDAEKQETGCPPLGL 120
Db 61 EQHVRIRVTKKKKVIKKKVKILTKRTPPLVTAGPLVTPPTAGTLPDAEKQETGCPPLGL 120
Qy 121 ESLRVSDSRLEASSSSQSGFLGPHRGRLNITQSGLEDGLYDGAWCAEQDADPMFQVDAGH 180
Db 121 ESLRVSDSRLEASSSSQSGFLGPHRGRLNITQSGLEDGLYDGAWCAEQDADPMFQVDAGH 180
Qy 181 PTFRFSGVITQGRNSVMRYDWTYSYKQFNSDRTWGSRNHSSGMDAVFPANSDPTPTVL 240
Db 181 PTFRFSGVITQGRNSVMRYDWTYSYKQFNSDRTWGSRNHSSGMDAVFPANSDPTPTVL 240
Qy 241 NLLPEQVARFIRLLPOTWLGQCAPCLRAEILACPVSDPNDLFLFAPASGSSDPLDFQHH 300
Db 241 NLLPEQVARFIRLLPOTWLGQCAPCLRAEILACPVSDPNDLFLFAPASGSSDPLDFQHH 300
Qy 301 NYKAMEKLMKQVQEQCPNITRIYSICKSYQGLKLYNMEMSDKPEHELGEPEVRYVAGMH 360
Db 301 NYKAMEKLMKQVQEQCPNITRIYSICKSYQGLKLYNMEMSDKPEHELGEPEVRYVAGMH 360

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Db 301 NYKAMKLMKQVBOQCPNITRIYSIGKSYOGLKLYVMEMSDKPGHEHGEPEVRVYAGMH 3 0
Qy 361 GNEALGRELLLLLMQFLCHEFLRGPNPRVTRLLSEMRHLLPSMNPDPGYEIAHRSSELVG 4 0
Db 361 GNEALGRELLLLLMQFLCHEFLRGPNPRVTRLLSEMRHLLPSMNPDPGYEIAHRSSELVG 4 0
Qy 421 WAEGRWNNQSIDLNHNFADLNTPLWEAODGKVPHTVNNHLLPLPTYYTLPNATVAPETR 4 0
Db 421 WAEGRWNNQSIDLNHNFADLNTPLWEAODGKVPHTVNNHLLPLPTYYTLPNATVAPETR 4 0
Qy 481 AVIKWMKRIPFVLSANLHGGELVVSYPFD----- 5 9
Db 481 AVIKWMKRIPFVLSANLHGGELVVSYPFD----- 5 9
Qy 510 ----- 5 9
Db 510 ----- 5 9
Qy 541 LAMODTSRRPCHSODFSVHGNIINGADWHTVPGSMNDFSYLHTNCFEVTVELSCDKFPHE 6 0
Qy 510 ----- 5 9
Db 601 NELPOEWENNKDALLTYLEQVRMGIAGVVRDKDTLGLIADAVIAVDGINHDVTTAWGGDY 6 0
Qy 510 -----WVTASAEVHSVTRNCRVTFEEGPPFCNPFVLTTPKORRELLAAGAKVPP 5 0
Db 661 WRLLTPGDYMVVTASAEVHSVTRNCRVTFEEGPPFCNPFVLTTPKORRELLAAGAKVPP 7 0
Qy 561 DLRRRLRLRGOKD 574
Db 721 DLRRRLRLRGOKD 734

RESULT 9
US-10-307-817-154
; Sequence 154, Application US/10307817
; Publication No. US20040058338A1
; GENERAL INFORMATION:
; APPLICANT: Agee et al.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-502C
; CURRENT APPLICATION NUMBER: US/10/307,817
; CURRENT FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 682
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 154
; LENGTH: 734
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-307-817-154

Query Match 97.1%; Score 2980; DB 15; Length 734;
Best Local Similarity 78.2%; Pred. No. 2, 2e-251;
Matches 574; Conservative 0; Mismatches 0; Indels 160; Gaps 1;

Qy 1 MWGLLLAALAAPAVAGPALGAPRNSVLGLAOPGTTKVPGSTPALHSSPAQPPAETANGTS 6'
Db 1 MWGLLLAALAAPAVAGPALGAPRNSVLGLAOPGTTKVPGSTPALHSSPAQPPAETANGTS 6'
Qy 61 EOHVRIRVTKKKVIMKKRKLTLTRPTPLVTAGPLVTPTAGTLDPAEKQETCCPLGL 1:0
Db 61 EOHVRIRVTKKKVIMKKRKLTLTRPTPLVTAGPLVTPTAGTLDPAEKQETCCPLGL 1:0
Qy 121 ESLRVSLSLEASSQSFGLGPHRGLNIOGLEDGDLVDGAWCAEEODADPWQVDACH 1:0
Db 121 ESLRVSLSLEASSQSFGLGPHRGLNIOGLEDGDLVDGAWCAEEODADPWQVDACH 1:0
Qy 181 PTRFSGVITCGNSVWRVYDWTYSYKVQFSDNRSRTWGSRNHSSGMDAVFPANSDPEFVL 2:0
Db 181 PTRFSGVITCGNSVWRVYDWTYSYKVQFSDNRSRTWGSRNHSSGMDAVFPANSDPEFVL 2:0
Qy 241 NLLPFPQVARTFRLLPOTWLOGGAPCLRAEILACVPSPDNDLFLFAPAGSGSDPLDFQHH 3:0
Db 241 NLLPFPQVARTFRLLPOTWLOGGAPCLRAEILACVPSPDNDLFLFAPAGSGSDPLDFQHH 3:0
```

```
Qy 301 NYKAMKLMKQVBOQCPNITRIYSIGKSYOGLKLYVMEMSDKPGHEHGEPEVRVYAGMH 360
Db 301 NYKAMKLMKQVBOQCPNITRIYSIGKSYOGLKLYVMEMSDKPGHEHGEPEVRVYAGMH 360
Qy 361 GNEALGRELLLLLMQFLCHEFLRGPNPRVTRLLSEMRHLLPSMNPDPGYEIAHRSSELVG 420
Db 361 GNEALGRELLLLLMQFLCHEFLRGPNPRVTRLLSEMRHLLPSMNPDPGYEIAHRSSELVG 420
Qy 421 WAEGRWNNQSIDLNHNFADLNTPLWEAODGKVPHTVNNHLLPLPTYYTLPNATVAPETR 480
Db 421 WAEGRWNNQSIDLNHNFADLNTPLWEAODGKVPHTVNNHLLPLPTYYTLPNATVAPETR 480
Qy 481 AVIKWMKRIPFVLSANLHGGELVVSYPFD----- 509
Db 481 AVIKWMKRIPFVLSANLHGGELVVSYPFD----- 509
Qy 510 ----- 509
Db 510 ----- 509
Qy 541 LAMODTSRRPCHSODFSVHGNIINGADWHTVPGSMNDFSYLHTNCFEVTVELSCDKFPHE 600
Qy 510 ----- 509
Db 601 NELPOEWENNKDALLTYLEQVRMGIAGVVRDKDTLGLIADAVIAVDGINHDVTTAWGGDY 660
Qy 510 -----WVTASAEVHSVTRNCRVTFEEGPPFCNPFVLTTPKORRELLAAGAKVPP 560
Db 661 WRLLTPGDYMVVTASAEVHSVTRNCRVTFEEGPPFCNPFVLTTPKORRELLAAGAKVPP 720
Qy 561 DLRRRLRLRGOKD 574
Db 721 DLRRRLRLRGOKD 734

RESULT 10
US-10-307-817-156
; Sequence 156, Application US/10307817
; Publication No. US20040058338A1
; GENERAL INFORMATION:
; APPLICANT: Agee et al.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-502C
; CURRENT APPLICATION NUMBER: US/10/307,817
; CURRENT FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 682
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 156
; LENGTH: 734
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-307-817-156

Query Match 97.1%; Score 2980; DB 15; Length 734;
Best Local Similarity 78.2%; Pred. No. 2, 2e-251;
Matches 574; Conservative 0; Mismatches 0; Indels 160; Gaps 1;

Qy 1 MWGLLLAALAAPAVAGPALGAPRNSVLGLAOPGTTKVPGSTPALHSSPAQPPAETANGTS 60
Db 1 MWGLLLAALAAPAVAGPALGAPRNSVLGLAOPGTTKVPGSTPALHSSPAQPPAETANGTS 60
Qy 61 EOHVRIRVTKKKVIMKKRKLTLTRPTPLVTAGPLVTPTAGTLDPAEKQETCCPLGL 120
Db 61 EOHVRIRVTKKKVIMKKRKLTLTRPTPLVTAGPLVTPTAGTLDPAEKQETCCPLGL 120
Qy 121 ESLRVSLSLEASSQSFGLGPHRGLNIOGLEDGDLVDGAWCAEEODADPWQVDACH 180
Db 121 ESLRVSLSLEASSQSFGLGPHRGLNIOGLEDGDLVDGAWCAEEODADPWQVDACH 180
Qy 181 PTRFSGVITCGNSVWRVYDWTYSYKVQFSDNRSRTWGSRNHSSGMDAVFPANSDPEFVL 240
Db 181 PTRFSGVITCGNSVWRVYDWTYSYKVQFSDNRSRTWGSRNHSSGMDAVFPANSDPEFVL 240
Qy 241 NLLPFPQVARTFRLLPOTWLOGGAPCLRAEILACVPSPDNDLFLFAPAGSGSDPLDFQHH 300
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Db 241 NLLPEQVAFIRLLPQTWLOGGAPCLRAEILACPVSDPNDLFLAEPASGSSDPLDFQHH 300
Qy 301 NYKAMRKLKMQVOEQCNITRIYSIGKSYOGLKLYVMEMSDKPGHEHLPGEPEVRYVAGMH 360
Db 301 NYKAMRKLKMQVOEQCNITRIYSIGKSYOGLKLYVMEMSDKPGHEHLPGEPEVRYVAGMH 360
Qy 361 GNEALGRELLLLMQFLCHEFLRGNPRVTRLLSEMRTHLLPSMNPDCGYEYAYHRGSELVG 420
Db 361 GNEALGRELLLLMQFLCHEFLRGNPRVTRLLSEMRTHLLPSMNPDCGYEYAYHRGSELVG 420
Qy 421 WAEGRWNNQSIDLNHNFPADLNTPLWEAQDDGKVPHIYPNHHLPPTYTYTLPNATVAPETR 480
Db 421 WAEGRWNNQSIDLNHNFPADLNTPLWEAQDDGKVPHIYPNHHLPPTYTYTLPNATVAPETR 480
Qy 481 AVIKMMKRIPFVLSANLHGELVVSYPFD----- 509
Db 481 AVIKMMKRIPFVLSANLHGELVVSYPFDMTRTPWAARELTPTPDDAVFRWLSTVYAGSN 540
Qy 510 ----- 509
Db 541 LAMQDTSRRPCHSQDSFVHGNIINGADWHTVPGSMNDFSYLHTNCFEVTVELSCDKFPHE 600
Qy 510 ----- 509
Db 601 NELPQEWENNKDALLTYLEQVRMGIAGVVRDKDTLGIADAVIADGINHDVTTAWGGDY 660
Qy 510 -----MVTASAGYHSVTRNCVTPFEGFPFCNFVLTCTPKQRLRELLAAGAKVPP 560
Db 661 WRLLTPGDYMTASAGYHSVTRNCVTPFEGFPFCNFVLTCTPKQRLRELLAAGAKVPP 720
Qy 561 DLRRRLRLRGQKD 574
Db 721 DLRRRLRLRGQKD 734

RESULT 11
US-09-813-432-38
; Sequence 38, Application US/09813432
; Publication No. US20030148485A1
; GENERAL INFORMATION:
; APPLICANT: Taupier Jr., Raymond J
; APPLICANT: Majmuder, Kamud
; APPLICANT: Spaderna, Steven K
; APPLICANT: Smithson, Glenda
; APPLICANT: Mezes, Peter S
; APPLICANT: Vernet, Corine A. M.
; TITLE OF INVENTION: No. US20030148485A1el Polypeptides and Amino Acids Encoding Same
; FILE REFERENCE: 15966-729
; CURRENT APPLICATION NUMBER: US/09/813,432
; PRIOR FILING DATE: 2001-03-20
; PRIOR FILING DATE: 2001-03-20
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 60/190,768
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 60/190,972
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/191,199
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/191,947
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/192,665
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,657
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,984
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,664
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,836
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/193,843
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 78

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38
; LENGTH: 734
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-813-432-38

Query Match 96.9%; Score 2976; DB 10; Length 734;
Best Local Similarity 78.1%; Pred. No. 4.9e-251;
Matches 573; Conservative 1; Mismatches 0; Indels 160; Gaps 1;

Qy 1 MWGLLLAALAPAPAVGALCAPNSVLGLAQPGTKKVPGSTPALHSSPAQPPAETANGTS 60
Db 1 MWGLLLAALAPAVGALCAPNSVLGLAQPGTKKVPGSTPALHSSPAQPPAETANGTS 60
Qy 61 EQHVRIRVIKKKKVIKKRKKLTLTRPTPLVATAGPLVTPTPAGTLPDPAEKOETGCPPLGL 120
Db 61 EQHVRIRVIKKKKVIKKRKKLTLTRPTPLVATAGPLVTPTPAGTLPDPAEKOETGCPPLGL 120
Qy 121 ESLRVSDSRLEASSQSFGLPGRGRNLNIOGLEDDGLYDGAWCABEQDADPWFQVDAGH 180
Db 121 ESLRVSDSRLEASSQSFGLPGRGRNLNIOGLEDDGLYDGAWCABEQDADPWFQVDAGH 180
Qy 181 PTRFSGVITQGRNSVMRYDWTYSYKQFSNDSRTWGSRNHSSGMDAVFPANSDPETPVL 240
Db 181 PTRFSGVITQGRNSVMRYDWTYSYKQFSNDSRTWGSRNHSSGMDAVFPANSDPETPVL 240
Qy 241 NLLPEQVAFIRLLPQTWLOGGAPCLRAEILACPVSDPNDLFLAEPASGSSDPLDFQHH 300
Db 241 NLLPEQVAFIRLLPQTWLOGGAPCLRAEILACPVSDPNDLFLAEPASGSSDPLDFQHH 300
Qy 301 NYKAMRKLKMQVOEQCNITRIYSIGKSYOGLKLYVMEMSDKPGHEHLPGEPEVRYVAGMH 360
Db 301 NYKAMRKLKMQVOEQCNITRIYSIGKSYOGLKLYVMEMSDKPGHEHLPGEPEVRYVAGMH 360
Qy 361 GNEALGRELLLLMQFLCHEFLRGNPRVTRLLSEMRTHLLPSMNPDCGYEYAYHRGSELVG 420
Db 361 GNEALGRELLLLMQFLCHEFLRGNPRVTRLLSEMRTHLLPSMNPDCGYEYAYHRGSELVG 420
Qy 421 WAEGRWNNQSIDLNHNFPADLNTPLWEAQDDGKVPHIYPNHHLPPTYTYTLPNATVAPETR 480
Db 421 WAEGRWNNQSIDLNHNFPADLNTPLWEAQDDGKVPHIYPNHHLPPTYTYTLPNATVAPETR 480
Qy 481 AVIKMMKRIPFVLSANLHGELVVSYPFD----- 509
Db 481 AVIKMMKRIPFVLSANLHGELVVSYPFDMTRTPWAARELTPTPDDAVFRWLSTVYAGSN 540
Qy 510 ----- 509
Db 541 LAMQDTSRRPCHSQDSFVHGNIINGADWHTVPGSMNDFSYLHTNCFEVTVELSCDKFPHE 600
Qy 510 ----- 509
Db 601 NELPQEWENNKDALLTYLEQVRMGIAGVVRDKDTLGIADAVIADGINHDVTTAWGGDY 660
Qy 510 -----MVTASAGYHSVTRNCVTPFEGFPFCNFVLTCTPKQRLRELLAAGAKVPP 560
Db 661 WRLLTPGDYMTASAGYHSVTRNCVTPFEGFPFCNFVLTCTPKQRLRELLAAGAKVPP 720
Qy 561 DLRRRLRLRGQKD 574
Db 721 DLRRRLRLRGQKD 734

RESULT 12
US-10-174-364-38
; Sequence 38, Application US/10174364
; Publication No. US20030216308A1
; GENERAL INFORMATION:
; APPLICANT: Anderson et al.
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-729CIP2
; CURRENT APPLICATION NUMBER: US/10/174,364

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; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: 60/190,835
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 60/190,768
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 60/190,972
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/191,199
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/191,947
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/192,665
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,657
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,984
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,664
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,836
; PRIOR FILING DATE: 2000-03-29
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38
; LENGTH: 734
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-174-364-38

Query Match          96.9%; Score 2976; DB 14; Length 734;
-Best Local Similarity 78.1%; Pred. No. 4.9e-251;
Matches 573; Conservative 1; Mismatches 0; Indels 160; Gaps 1;

QY      1 MWGLLLAALAAPAVGAPALCAPRNSVLGLAOPGTTKVPGSTPALHSSPAQPPAETANGTS 6(
DB      1 MWGLLLAALAAPAVGAPALCAPRNSVLGLAOPGTTKVPGSTPALHSSPAQPPAETANGTS 6(
QY      61 EQHVRIRVIKKKVIKKRKKLLTRPTPLVTAAGPLVTPAGTLDPAEKQSTGCPPLGL 1(
DB      61 EQHVRIRVIKKKVIKKRKKLLTRPTPLVTAAGPLVTPAGTLDPAEKQSTGCPPLGL 1(
QY      121 ESLRVSLSRLAASSOSFGLGPHRGRNLNQSGLDGLDYGAWCAEEQDADPWFQVDAGH 1(
DB      121 ESLRVSLSRLAASSOSFGLGPHRGRNLNQSGLDGLDYGAWCAEEQDADPWFQVDAGH 1(
QY      181 PTRFSGVITQGRNSVVRWDVTSYKVFQNSDRTWWSNRHSSGMDVFPANSDETPVL 24(
DB      181 PTRFSGVITQGRNSVVRWDVTSYKVFQNSDRTWWSNRHSSGMDVFPANSDETPVL 24(
QY      241 NLLPEQVAFRLLPQWLQGAFCPLRAEILACPVSDPNDLFLAPASGSDPLDPQHH 30(
DB      241 NLLPEQVAFRLLPQWLQGAFCPLRAEILACPVSDPNDLFLAPASGSDPLDPQHH 30(
QY      301 NYKAMEKLMKQVQEQCPNITRIYSTGKSYOGKLYVMEMSDKGGHELGEPEVRYVAGMH 36(
DB      301 NYKAMEKLMKQVQEQCPNITRIYSTGKSYOGKLYVMEMSDKGGHELGEPEVRYVAGMH 36(
QY      361 GNEALGRELLLLMQFLCHEFLRGHPVTRLLSEMRHLLFSMNDPDGYEIAHYRGSSELVG 42(
DB      361 GNEALGRELLLLMQFLCHEFLRGHPVTRLLSEMRHLLFSMNDPDGYEIAHYRGSSELVG 42(
QY      421 WAEGRWNNQSIDLNNFADNLPLNEAODDGKPHIVFNHLLPLPTYYTLNATVAPETR 48(
DB      421 WAEGRWNNQSIDLNNFADNLPLNEAODDGKPHIVFNHLLPLPTYYTLNATVAPETR 48(
QY      481 AVIKMKRIPFVLSANLGGELVSVSPD-----50(
DB      481 AVIKMKRIPFVLSANLGGELVSVSPD-----50(
QY      510 -----50(
DB      541 LAMQDTSRRPCHSQDPFSVHGNIINGADWHVTVPGSMDFSYLHNCFEVTVLSCDKFPHE 60(
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QY      510 -----50(
DB      601 LAMQDTSRRPCHSQDPFSVHGNIINGADWHVTVPGSMDFSYLHNCFEVTVLSCDKFPHE 660
QY      510 -----MTTASAGVSHSVTRNCRVTFEEGFFFCNFVLTTPKQRLRELIAAGAKVPP 560
DB      661 WRLLTPGDYMTTASAGVSHSVTRNCRVTFEEGFFFCNFVLTTPKQRLRELIAAGAKVPP 720
QY      561 DLRRLRLRGQKD 574
DB      721 DLRRLRLRGQKD 734
```

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RESULT 13
US-10-246-583-38
; Sequence 38, Application US/10246583
; Publication No. US20040058862A1
; GENERAL INFORMATION:
; APPLICANT: Majumder
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-729CIP2CON1
; CURRENT APPLICATION NUMBER: US/10/246,583
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: 10/174,364
; PRIOR FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: 60/190,835
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 60/190,768
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 60/190,972
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/191,199
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/191,947
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/192,665
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,657
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,984
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,664
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38
; LENGTH: 734
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-246-583-38
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Query Match          96.9%; Score 2976; DB 15; Length 734;
-Best Local Similarity 78.1%; Pred. No. 4.9e-251;
Matches 573; Conservative 1; Mismatches 0; Indels 160; Gaps 1;

QY      1 MWGLLLAALAAPAVGAPALCAPRNSVLGLAOPGTTKVPGSTPALHSSPAQPPAETANGTS 60(
DB      1 MWGLLLAALAAPAVGAPALCAPRNSVLGLAOPGTTKVPGSTPALHSSPAQPPAETANGTS 60(
QY      61 EQHVRIRVIKKKVIKKRKKLLTRPTPLVTAAGPLVTPAGTLDPAEKQSTGCPPLGL 120(
DB      61 EQHVRIRVIKKKVIKKRKKLLTRPTPLVTAAGPLVTPAGTLDPAEKQSTGCPPLGL 120(
QY      121 ESLRVSLSRLAASSOSFGLGPHRGRNLNQSGLDGLDYGAWCAEEQDADPWFQVDAGH 180(
DB      121 ESLRVSLSRLAASSOSFGLGPHRGRNLNQSGLDGLDYGAWCAEEQDADPWFQVDAGH 180(
QY      181 PTRFSGVITQGRNSVVRWDVTSYKVFQNSDRTWWSNRHSSGMDVFPANSDETPVL 240(
DB      181 PTRFSGVITQGRNSVVRWDVTSYKVFQNSDRTWWSNRHSSGMDVFPANSDETPVL 240(
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241 NLLPEQVAFIRLLPQTLQGGAPCLRAEILACPVSDPNDLFLAPASGSSDPLDFQHH 300
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301 NYKAMEKLMKQVQEQCPNITRIYSIGKSYQGLKLYMNSDKGEHELGEPEVRYVAGMH 360
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361 GNEALGRELILLMLQFLCHEFLRGNPRVTRLISEMRTHLLPSMNPQGYEYAYHRGSELVG 420
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421 WAEGRWNNQSIDLNHNFDLNTPLWBAQDDGKVPVHVPNNHLLPLPTYYTLPNATVAPETR 480
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561 DLRRRLRLRGQKD 574
721 DLRRRLRLRGQKD 734

RESULT 14

US-10-689-832-38
; Sequence 38, Application US/10689832
; Publication No. US20040121380A1
; GENERAL INFORMATION:
; APPLICANT: Majmuder, Kamud
; TITLE OF INVENTION: Novel Polypeptides and Amino Acids Encoding Same
; FILE REFERENCE: 15966-729DIV1
; CURRENT APPLICATION NUMBER: US/10/689, 832
; CURRENT FILING DATE: 2003-10-20
; PRIOR APPLICATION NUMBER: 09/813,432
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/190,835
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 60/190,768
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 60/190,972
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/191,199
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/191,947
; PRIOR FILING DATE: 2000-03-24
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; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,657
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,984
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,664
; PRIOR FILING DATE: 2000-03-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38
; LENGTH: 734
; TYPE: PRT

; ORGANISM: Homo sapiens
US-10-689-832-38
Query Match 96.9%; Score 2976; DB 16; Length 734;
Best Local Similarity 78.1%; Pred. No. 4.9e-251; Indels 160; Gaps 1;
Matches 573; Conservative 1; Mismatches 0;
QY 1 MWGLLLAALFAVPAVGPALGAPRNSVLGLAQPOCTTKVPGSTPALHSSPAQPAETANGTS 60
DB 1 MWGLLLAALFAVPAVGPALGAPRNSVLGLAQPOCTTKVPGSTPALHSSPAQPAETANGTS 60
QY 61 EQHVRIRVTKKKKVINKKRKKLTLTRPTPLVTAAGPLVTPPTAGTLPDAEKQETGCPPLGL 120
DB 61 EQHVRIRVTKKKKVINKKRKKLTLTRPTPLVTAAGPLVTPPTAGTLPDAEKQETGCPPLGL 120
QY 121 ESURVSDSRLSEASSSSQFGLGPHRGRNLNQSGLDGLYDGCACAEQDADPFQVDAGH 180
DB 121 ESURVSDSRLSEASSSSQFGLGPHRGRNLNQSGLDGLYDGCACAEQDADPFQVDAGH 180
QY 181 PTRFSGVITQGRNSVMRYDWTISYKVQFSNDSRTWMSRHHSSGMDAVFPANSDPETPVL 240
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QY 301 NYKAMEKLMKQVQEQCPNITRIYSIGKSYQGLKLYMNSDKGEHELGEPEVRYVAGMH 360
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DB 361 GNEALGRELILLMLQFLCHEFLRGNQVTRLISEMRTHLLPSMNPQGYEYAYHRGSELVG 420
QY 421 WAEGRWNNQSIDLNHNFDLNTPLWBAQDDGKVPVHVPNNHLLPLPTYYTLPNATVAPETR 480
DB 421 WAEGRWNNQSIDLNHNFDLNTPLWBAQDDGKVPVHVPNNHLLPLPTYYTLPNATVAPETR 480
QY 481 AVIKMKRIPFVLSANLHGELVVSYPFD----- 509
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DB 721 DLRRRLRLRGQKD 734
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US-10-052-586-458
; Sequence 458, Application US/10052586
; Publication No. US20020127584A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria

APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3430R1C1
CURRENT APPLICATION NUMBER: US/10/052,586
CURRENT FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR APPLICATION NUMBER: 60/089105
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; PRIOR APPLICATION NUMBER: 60/089653
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089908

Query Match          96.9%; Score 2975; DB 13; Length 734;
Best Local Similarity 78.1%; Pred. No. 6e-251;
Matches 573; Conservative 0; Mismatches 1; Indels 160; Gaps 1;

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Db 1 MWGLLLALAAPAVGAPALGAPRNSVLGLAQPGTTKYPGSTPALHSSPAQPPAETANGTS 60

Qy 61 EQHVRIRVIKKKVIKKRKKLTLTRPTPLVTAGPLVTPPTAGTLPDAEKQETGCPPLGL 120
Db 61 EQHVRIRVIKKKVIKKRKKLTLTRPTPLVTAGPLVTPPTAGTLPDAEKQETGCPPLGL 120

Qy 121 ESLRVSLSLEASSQSFGLPGRGRNLIOSGLEDDGLYDGAMCABEQDADPMFQVDAGH 180
Db 121 ESLRVSLSLEASSQSFGLPGRGRNLIHISGLEDDGLYDGAMCABEQDADPMFQVDAGH 180

Qy 181 PTRFSGVITQGRNSVMRYDWTYSKYQFSDNSRTWGSNRHSSGMDAVFPANSDPETPVL 240
Db 181 PTRFSGVITQGRNSVMRYDWTYSKYQFSDNSRTWGSNRHSSGMDAVFPANSDPETPVL 240

Qy 241 NLLPEQOVARFIRLLPOTWLOGGAPCLRABILACPVSDPDNDLFLEAPAGSSDPLDFQHH 300
Db 241 NLLPEQOVARFIRLLPOTWLOGGAPCLRABILACPVSDPDNDLFLEAPAGSSDPLDFQHH 300

Qy 301 NYKAMRKLKMQOECQCNITRIYSIGKSYOGLKLYMMSDKPGEHELGEPEVRYVAGMH 360
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Qy 510 -----MVTASAEGYHSVTRNCRVTFEEGPPPCNFVLTKTKQRLRELLAAGAKVPP 560
Db 661 WRLLTPGDYMTASAEGYHSVTRNCRVTFEEGPPPCNFVLTKTKQRLRELLAAGAKVPP 720
Qy 561 DLRRRLRLRGQKD 574
Db 721 DLRRRLRLRGQKD 734
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 10, 2005, 19:28:10 ; Search time 43 Seconds
(without alignments)
1284.382 Million cell updates/sec

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Perfect score: 3070
Sequence: 1 MWGILLALAAFAFAPVGPALG.....GAKVPPDLRRRLRLRGQKD 574

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1071.5	34.9	719	2 S51739	transcription repr
3	616	20.1	458	2 S02074	lysine carboxypepc
4	582.5	19.0	454	2 A54324	carboxypeptidase H
5	579	18.9	476	2 S12461	carboxypeptidase E
6	579	18.9	476	2 A40469	carboxypeptidase E
7	574	18.7	476	2 S09489	carboxypeptidase E
8	564	18.4	448	2 A24327	carboxypeptidase E
9	563.5	18.4	477	2 S16383	carboxypeptidase E
10	495.5	16.1	1389	2 T50090	carboxypeptidase g
11	458.5	14.9	1446	2 T30916	carboxypeptidase D
12	439.5	14.3	1119	2 T13284	carboxypeptidase (
13	439.5	14.3	1404	2 T13420	probable carboxype
14	439.5	14.3	1406	2 T13421	probable carboxype
15	431	14.0	472	2 T20454	hypothetical prote
16	415	13.5	985	2 T29910	hypothetical prote
17	402.5	13.1	439	2 A32619	carboxypeptidase M
18	400.5	13.0	501	2 T25343	hypothetical prote
19	351	11.4	491	2 B96739	hypothetical prote
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21	249	8.1	427	2 JC4915	ags protein precu
22	248	8.1	463	1 A36479	milk fat globule m
23	236.5	7.7	2183	2 T42764	coagulation factor
24	229.5	7.5	2211	1 KFB05	coagulation factor
25	227	7.4	409	2 T11743	pp47 protein - pig
26	224.5	7.3	2224	1 KFHU5	coagulation factor
27	224	7.3	2133	2 T42763	coagulation factor
28	221	7.2	401	2 S65138	glycoprotein antig
29	221	7.2	427	2 S74211	PAS-6/7 protein pr

30	217	7.1	216	2 A44258	factor VIII-associ
31	217	7.1	2319	2 A47004	coagulation factor
32	217	7.1	2351	1 EZHU	coagulation factor
33	201	6.5	424	2 S17571	carboxypeptidase T
34	190.5	6.2	999	2 T36021	probable zinc-bind
35	181.5	5.9	913	2 A48280	receptor tyrosine k
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37	180.5	5.9	876	2 A49508	protein-tyrosine k
38	180.5	5.9	927	1 JQ0948	A5 antigen precu
39	180	5.9	451	2 S20723	carboxypeptidase (
40	178.5	5.8	910	2 A53137	tyrosine kinase re
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42	170.5	5.6	528	2 T33527	hypothetical prote
43	162.5	5.3	819	2 I48859	tyro 10 receptor k
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ALIGNMENTS

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C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: JC5256
R;Ohno, I.; Hashimoto, J.; Shimizu, K.; Takaoka, K.; Ochi, T.; Matsubara, K.; Okubo, K.
Biochem. Biophys. Res. Commun. 228, 411-414, 1996
A;Title: A cDNA cloning of human AEBP1 from primary cultured osteoblasts and its express
A;Reference number: JC5256; MUID:97079196; PMID:8920928
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A;Molecule type: mRNA
A;Residues: 1-845 <OHN>
A;Cross-references: UNIPROT:Q14113; DDBJ:D86479; NID:g1468942; PIDN:BAA13094.1; PID:g146

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DB	183	-TFHGNVDKDTPLVSELPEPVARFIRIYPLTW--NGSLCNRLEVLGCSVAPVSYVAQN	239
QY	287	PASGSDPLDFQHNYKAMKLMKQVQECPNITRIYSIGSKYQGLKLYVMESDKPGEH	346
DB	240	EVV-ATDDLDFRHSYKDMRQLMKVWNECPTITRTYSLGKSRGLKIYAMEISDNDEH	298
QY	347	ELGEPEVRYVAGMHGNEALGREILLILMQFLCHEFRGNPRVTRLLSEMIHLIPSNPD	406
DB	299	ELGEPEFRYTAGTHGNEVLGRELLILMQYLCREYRDGNPRVSLVQDTRIHLVPSLNPD	358
QY	407	GYEIAVHRGSELVGAEGRWNNOSIDLNNHFNADLNTPLWEAODDGKVPHTVPNNHLLPPT	466
DB	359	GYEVAQMGSEFGNWLGLWTEGDFIDFDPDLNSVLNGABERKWKVPRVPPNNLPIPE	418
QY	467	YYTLPNATVAPETRAVIKWMKRIPFVLSANLHGELVVSYPFDM-----	510
DB	419	RYLSPDATVSTEVRAIIAWMEKPPFVLGNLNGERLVSYPYDMARTPTQQLAAAMAA	478
QY	511	-----	510
DB	479	ARGEDEVSEAQETPDHAIFRWLAISFASAHILTLEPYRGCGQAQDYTGGMIVNGAKW	538

QY 511 ----- 510
Db 539 NPRTGTINDFSYLHNTCLSELSFYLGCDFPHESELPREWENKREALLTFMEQVHRGKGV 598
QY 511 -----VTASAEGYHSVTRNCRCVTF 529
Db 599 VTDEQGIPIANATISVSGINHGVKTASGGDYWRILNPCEYRVTAHAGYTPSAKTQNDVY 658
QY 530 BEGPPFCNFVLTKTPKQRLRELLAAGAKVP -----PDLR-----RLRG 571
Db 659 DIGATQCNCFILARNWKKRIREIMAMNGNRPPIPHIDPSRPMTPQQRRLQORRLQRLRLRA 718
QY 572 Q 572
Db 719 Q 719

RESULT 2
SS1739
A:Title: transcription repressor AEBP1 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
A:Accession: S60227; SS1739
R:He, G.P.; Muise, A.; Li, A.W.; Ro, H.S.
Nature 378, 92-96, 1995
A:Title: A eukaryotic transcriptional repressor with carboxypeptidase activity.
A:Reference number: S60227; MUID:96061010; PMID:7477299
A:Accession: S60227
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-719 <HE2>
A:Cross-references: UNIPROT:Q61281; EMBL:X80478; NID:9607131; PIDN:CAA56648.1; PID:g6071

Query Match 34.98; Score 1071.5; DB 2; Length 719;
Best Local Similarity 36.87; Pred. No. 7.5e-73;
Matches 224; Conservative 68; Mismatches 123; Indels 193; Gaps 5;

QY 149 IQSGLEDGLYDGAWCAEEQDADPWFOVDAGHPTFSGVITQGRNSVWRVYDWTSYKVOF 208
Db 1 MQAGANEDDYDGAWCAEDSESQTQWLEVDTRRTTGTGVTQGRDSIHDDFTVTFVGF 60
QY 209 SndsRTWGRNSHSSGNDVAFVANSDEPTVLLNLLPEQVAVRIRLLPOTVIGGAPCLR 268
Db 61 SndsQTVWMTYNGEEM--TFYGNVDKTPVLSELPEPVVARIYIPLTW--NGSLCWR 116
QY 269 AEILACPVDNDLFLEAPASGSSDPLDFOHNYKAMRKLMKQVQOCNTRIYSIGKS 328
Db 117 LEVLGCEVTPVYSYQAQNEVV--TTSDLDPRHSYKDMRQMKAVNEECPTIIRTSYLGKS 175
QY 329 YQGLKLYVWMSDKPGEHELGEPEVRYVAGMHGNEALGRELLLLMQFLCHFEFLRGNPRV 388
Db 176 SRGLKIYAMEISDNPGDHELGEPEFRYTAGIHGNEVLGRELLLLMQYLCOEYRDGNPRV 235
QY 389 TRLLSEWRHLLPSMNPDPGYEYAYHGRSELVWAGRWNNQSIDLNHNFPADLNTPLWEAQ 448
Db 236 RNLVQDTRHLVPSLNPDPGYEYAAQMGSEFGNWLGLMTTEEGFDIFEDFPDLNSVLWAAE 295
QY 449 DQGVPHIVPNHLLPLPTTYTLPNATVAPETRAVIKMKRIPFVLSANLHGELVVSYPF 508
Db 296 EKKWVYRVNPNLPIPERYLPDQATVSTEVRAIISWKEKNPFVLGANGLNGERLVSIPY 355
QY 509 DM----- 510
Db 356 DMARTSQQLAEALAAARGDDGVSBAQETPDPAIFRWLAISFASAHLTMTPEYRG 415
QY 511 ----- 510
Db 416 CQAQDYTCGMGIVNGAKWNPRTGTFNDPSYLTNCLSELSVYLGCDKFPHESELPREWENN 475
QY 511 -----V 511
Db 476 KEALLTFMEQVHRGKGVVTDQGIPIANATISVSGINHGVKTASGGDYWRILNPGEYRV 535

QY 512 TASAEGYHSVTRNCRCVTFEFGPPFCNFVLTKTPKQRLRELLAAGAKVP -----P 560
Db 536 TAAHAGYTSACKNCVDYDIGATQCNCFILARNWKKRIREILLAMNGNRPILRVDPSPRPMP 595
QY 561 DLRRLER 568
Db 596 QQRMRQOR 603

RESULT 3
S02074

lysine carboxypeptidase (EC 3.4.17.3) small chain precursor - human
N:Alternate names: anaphylatoxin inactivator small subunit; carboxypeptidase N small subunit
C:Species: Homo sapiens (man)
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
A:Accession: S02074

R:Gebhard, W.; Schube, M.; Eulitz, M.

Eur. J. Biochem. 178, 603-607, 1989

A:Title: cDNA cloning and complete primary structure of the small, active subunit of human
N:Reference number: S02074; MUID:89107181; PMID:2912725

A:Accession: S02074

A:Molecule type: mRNA

A:Residues: 1-458 <GB>

A:Cross-references: UNIPROT:P15169; EMBL:X14329; NID:g30296; PIDN:CAA32507.1; PID:g30297
A:Note: part of this sequence, including the amino end of the mature protein, was confirmed
C:Superfamily: human carboxypeptidase H

C:Keywords: hydrolase; metallo-carboxypeptidase

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-458/Product: lysine (arginine) carboxypeptidase small chain #status experimental <M

Query Match 20.11; Score 616; DB 2; Length 458;

Best Local Similarity 48.11; Pred. No. 1e-38;

Matches 125; Conservative 36; Mismatches 75; Indels 24; Gaps 4;

QY 294 PLDFOHNYKAMRKLMKQVQOCNTRIYSIGKSQGLKLYWMSDKPGEHELGEPEV 353
Db 20 PVTFRHRYDDLVTLLYKQNECGITRVYSIGSVGRHLVLEFSDHPGHEPLEPEV 79

QY 354 RYVAGMHGNEALGRELLLLMQFLCHFEFLRGNPRVTRLLSEMRHLLPSMNPDPGYEYAYH 413
Db 80 KYVGMHGEALGRELMQLSEFLCEEFNRNRQIRVQLIQTRIHLPSMNPDPGYEYAAA 139

QY 414 RGSSELVWAGRWNNQSIDLNHNFPADLNTPLWEAQDQGVPHIVPNHLLPLPTTYTLPNA 473
Db 140 QGNPKPGVLGRNNAVGVNPPDNTIYNEKYGG-----PNHLLPLDNW---KS 191

QY 474 TVAPETRAVIKMKRIPFVLSANLHGELVVSYPFDMVTASAGYHSVTRNCRCVTFEEGP 533
Db 192 QVEPETRAVIRWMSFNFLSANLHGGAVVANPYD-----KSFEHRVGRVART----- 240

QY 534 FPCNFVLTKTPKQRLRELLA 553

Db 241 -----ASTPTDDPKLFQKLA 255

RESULT 4
A54324

carboxypeptidase H - American goosefish

C:Species: Lophius americanus (American goosefish)

C:Date: 29-Aug-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

A:Accession: A54324

R:Roth, W.W.; Mackin, R.B.; Spies, J.; Goodman, R.H.; Noe, B.D.

Mol. Cell. Endocrinol. 78, 171-178, 1991

A:Title: Primary structure and tissue distribution of anglerfish carboxypeptidase H.

A:Reference number: A54324; MUID:92137483; PMID:1778303

A:Accession: A54324

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-454 <ROT>

A:Cross-references: UNIPROT:P37892; GB:S80565; NID:g244402; PIDN:AAA03252.1; PID:g244403

A:Note: sequence extracted from NCBI backbone (NCBIN:80565, NCBI:P:80566)

C:Superfamily: human carboxypeptidase H

C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
C;Accession: S09489
R;Manser, E.; Fernandez, D.; Loo, L.; Goh, P.Y.; Monfries, C.; Hall, C.; Lim, L.
Biochem. J. 267, 517-525, 1990
A;Title: Human carboxypeptidase E. Isolation and characterization of the cDNA, sequence
A;Reference number: S09489; MUID:90241164; PMID:2334405
A;Accession: S09489
A;Molecule type: mRNA
A;Residues: 1-476 <MAN>
A;Cross-references: UNIPROT:P16870; EMBL:X51405; NID:g29666; PIDN:CAA35767.1; PID:g29667
C;Genetics:
A;Gene: GDB:CPE
A;Cross-references: GDB:127894; OMIM:114855
A;Map position: 4pter-4qter
C;Superfamily: human carboxypeptidase H
C;Keywords: hydrolase; metallo-carboxypeptidase

Query Match 18.7%; Score 574; DB 2; Length 476;
Best Local Similarity 44.4%; Pred. No. 1.7e-35;
Matches 116; Conservative 47; Mismatches 76; Indels 22; Gaps 6;
QY 271 ILACPVSDNDLFLAPASG-----SSDPLDFQHHNYKAMRKLKMQVQEQCPNITRI 322
Db 22 LLGAQAQPG-----APAGWRRRRRLQEDGISFEYHRYPELREALVSVWLQCTAISRI 76
QX 323 YISGYSQGLKLYNEMSKDGEHELGEPEVRYVAGMGNALGRELLELLLMQFLCHEFL 382
Db 77 YTVGRSFEGRLELLVIELSDNPGVHEPEPEPKYIGNMHNENAVGRELLELLIFLAQYLCNEVQ 136
QY 383 RGNPRVTRLLSEMRIHLLPSNPDGYEIAVHRGSELVGMWAEGRWNNQSIDLNHNFPDLNT 442
Db 137 KGNETIVNLHSTRHIMPSLNPDGFEKAASQGLKDFVGRSNAQGDIDLRNFPDLOR 196
QY 443 PLWEAQDDGKVPHPVPHLPLPTYYTL--PNATVAPETRAVIKWKMKRIPFVLSANLHGG 500
Db 197 IVVYNEKEGG-----PNHL-LKNKKIVDQNTKLAPETRAVIHIMDIPEVLSANLHGG 250
QY 501 ELVSVSPFDMV-TASAEGYHS 520
Db 251 DLVANYPYDTRSGSAHEYSS 271

RESULT 8
A24327
carboxypeptidase E (EC 3.4.17.10) 56K chain - bovine
N;Alternate names: carboxypeptidase E; enkephalin convertase; glycoprotein J; glycoprotein J; glycoprotein J
C;Contains: Bos primigenius taurus H 53K chain
C;Species: Bos primigenius taurus (cattle)
C;Date: 21-May-1988 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004
C;Accession: A24327; S11467; S11466; A30305; B38305
R;Fricker, L.D.; Evans, C.J.; Esch, F.S.; Herbert, E.
Nature 323, 461-464, 1986
A;Title: Cloning and sequence analysis of cDNA for bovine carboxypeptidase E.
A;Reference number: A24327; MUID:87014809; PMID:3020433
A;Accession: A24327
A;Molecule type: mRNA
A;Residues: 15-448 <FRI>
A;Cross-references: UNIPROT:P04836; GB:X04411; NID:g279; PIDN:CAA27999.1; PID:g1364188
R;Christie, D.L.; Palmer, D.J.
Biochem. J. 270, 57-61, 1990
A;Title: Identification and characterization of glycoproteins after extraction of bovine fraction.
A;Reference number: S11466; MUID:90372935; PMID:2396993
A;Accession: S11467
A;Molecule type: protein
A;Residues: 1-22 <CHR>
A;Accession: S11466
A;Molecule type: protein
A;Residues: 'X', '16-23', 'G', <CH2>
R;Parkinson, D.
J. Biol. Chem. 265, 17101-17105, 1990
A;Title: Two soluble forms of bovine carboxypeptidase H have different NH-2-terminal sequences.
A;Reference number: A38305; MUID:91009137; PMID:2211611

A;Note: presence of carboxyl terminal peptide was confirmed by monoclonal antibody
A;Accession: A38305
A;Molecule type: protein
A;Residues: 1-4, 'X', '6-10', 'R' <PAR>
A;Accession: B38305
A;Molecule type: protein
A;Residues: 'X', '16-33' <PA2>
C;Superfamily: human carboxypeptidase H
C;Keywords: hydrolase; metallo-carboxypeptidase; zinc
F;1-448/Product: carboxypeptidase H 56K chain #status experimental <MAT>
F;15-448/Product: carboxypeptidase H 53K chain #status experimental <MA2>
F;86,89,220/Binding site: zinc (His, Glu, His) #status predicted
F;292,314/Active site: Tyr, Glu #status predicted

Query Match 18.4%; Score 564; DB 2; Length 448;
Best Local Similarity 45.5%; Pred. No. 8.6e-35;
Matches 111; Conservative 48; Mismatches 69; Indels 16; Gaps 5;
QY 287 PASGS-----SDPLDFQHHNYKAMRKLKMQVQEQCPNITRIYSIGKSYQGLKLYVEM 339
Db 6 PVAGAGRRXRQEDGISFEYHRYPELREALVSVWLQCAAVSRIYVGRSEFGRLELLVLEL 65
QY 340 SDKPCEHELGEPEVRYVAGMGNALGRELLELLLMQFLCHEFLRGNPRVTRLLSEMRIHL 399
Db 66 SDNPGVHEPEPEPKYIGNMHNENAVGRELLELLIFLAQYLCNEYKGNETIVQLHNTRIHI 125
QY 400 LPSMNPDPGYEIAVHRGSELVGMWAEGRWNNQSIDLNHNFPDLNTPLWEAQDDGKVPHPV 459
Db 126 MFSLNPDGFEKAASQGLKDFVGRSNAQGDIDLRNFPDLDRIVYINEKEGG-----PN 180
QY 460 HHLPLPTYYTL--PNATVAPETRAVIKWKMKRIPFVLSANLHGGELVSVSPFDMV-TASAE 516
Db 181 NHL-LKNKKIVDQNTKLAPETRAVIHIMDIPEVLSANLHGGDLVANYPYDTRSGSAH 239
QY 517 GYHS 520
Db 240 EYSS 243

RESULT 9
S16383
carboxypeptidase E (EC 3.4.17.10) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S16383
R;Parkinson, D.
submitted to the EMBL Data Library, August 1991
A;Description: Mutational analysis of the sorting signal for carboxypeptidase H.
A;Reference number: S16383
A;Accession: S16383
A;Molecule type: mRNA
A;Residues: 1-477 <PAR>
A;Cross-references: UNIPROT:Q00493; EMBL:X61232; NID:g50312; PIDN:CAA43550.1; PID:g50313
C;Superfamily: human carboxypeptidase H
C;Keywords: hydrolase; metallo-carboxypeptidase

Query Match 18.4%; Score 563.5; DB 2; Length 477;
Best Local Similarity 45.5%; Pred. No. 1e-34;
Matches 112; Conservative 47; Mismatches 70; Indels 17; Gaps 5;
QY 286 APASG-----SSDPLDFQHHNYKAMRKLKMQVQEQCPNITRIYSIGKSYQGLKLYVEM 337
Db 32 APAAGWRRRRRLQEDGISFEYHRYPELREALVSVWLQCTAISRIYVGRSEFGRLELLVI 91
QY 338 EMSDKPGEHELGEPEVRYVAGMGNALGRELLELLLMQFLCHEFLRGNPRVTRLLSEMRI 397
Db 92 ELSDNPGVHEPEPEPKYIGNMHNENAVGRELLELLIFLAQYLCNEYKGNETIVNLHSTRI 151
QY 398 HLLPSMNPDPGYEIAVHRGSELVGMWAEGRWNNQSIDLNHNFPDLNTPLWEAQDDGKVPHPV 457
Db 152 HIMPSLNPDGFEKAASQGLKDFVGRSNAQGDIDLRNFPDLDRIVYINEKEGG----- 206
QY 458 PNHLPLPTYYTL--PNATVAPETRAVIKWKMKRIPFVLSANLHGGELVSVSPFDMV-TAS 514

Db 207 PNNHL-LKNLKKIVDQNSKLAPETKAVIHWIMDIPFVLNSANLHGDLVANYPYDETRSGT 265
Qy 515 AEGYHS 520
Db 266 AHEYSS 271
RESULT 10
I50090
carboxypeptidase gp180 - Anas sp.
C;Species: Anas sp.
C;Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 09-Jul-2004
R;Kuraki, K.; Eng, F.; Ishikawa, T.; Turck, C.; Harada, F.; Ganem, D.
J. Biol. Chem. 270, 15022-15028, 1995
A;Title: gp180, a host cell glycoprotein that binds duck hepatitis B virus particles, is
A;Reference number: A57010; MUID:93118059; PMID:17797483
A;Accession: I50090
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-1389 <KUR>
A;Cross-references: UNIPROT:Q90240; EMBL:U25126; NID:g1008477; PIDN:AAA78903.1; PID:g1008477
Query Match 16.1%; Score 495.5; DB 2; Length 1389;
Best Local Similarity 31.1%; Pred. No. 6.5e-29;
Matches 133; Conservative 60; Mismatches 112; Indels 123; Gaps 18;
Qy 154 EDGDLY-DGAWCAEQADPWQVDAGHPTRFSCVITQGRNSVWRVDTSYKQVF---- 208
Db 315 EGETFDQGI-----TNGAQWYVEGQM-----YNYVMANCFEITLSC 356
Qy 209 -----SNDSTWWSGRNHS-----SGM--DAVFPANSDPETPVL-----NLLPE 245
Db 357 CKYPTSELQOEWHNRESLLTFIEKVHIGVKGEVRDAITGAGLENATIVVAGIAHNTA 416
Qy 246 PQVAFIRLL-PQW-----LOGGAPCLRAEI-----LACPVSDDN-D 281
Db 417 GKFGDHRLLVPGTYNVTAVVMGYAPVTKENIEVKADATWDFSLQPTVAP--DPNLT 474
Qy 282 LFLAPASGSS-----DPLDFOHNYKAMKMLKMQVQPCNITR 321
Db 475 QFTATPAPPSTLTPSVAQVEPPATTSLHQAVQVPVDFRHHFSOMEIPLRYAYEYSITR 534
Qy 322 IYSGIKSYQGLKLYVMMSDKPGHELGEPVRYVAGMHGNEALGRELLLLMQFLCHEF 381
Db 535 LYSVGKSVRELXYMEISNPGIHEAGEPEFKYIGNMHGNEVVVGRELLNLEILCKNP 594
Qy 382 LRGNPRVTRLLSEMRHLLPSMNPDPGYEIAHYHRSSELVWGAEGRWNNSIDLHNFADLN 441
Db 595 -GTDPEVTDLVQSTRIHMFMSMNPDPGYEKS-QEGDR--GQTVGRNNSNYDLNRNFPD-- 648
Qy 442 TPLWEAQDDGKVPHVPNHHLPLPTYYTLPNATVAPETRAVIKMKRIPFVLSANLHGGE 501
Db 649 -QFQVTDPPQ-----PETLVMGSLKTYPPFVLSANLHGGS 683
Qy 502 LVVSYPPD 509
Db 684 LVVNYPPD 691
RESULT 11
T30916
carboxypeptidase D (EC 3.4.17.-) - California sea hare
C;Species: Aplysia californica (California sea hare)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
R;Fan, X.; Qian, Y.; Fricker, L.D.; Akatal, D.B.; Nagle, G.T.
DNA Cell Biol. 18, 121-132, 1999
A;Title: Cloning and expression of Aplysia carboxypeptidase D, a candidate prohormone-
A;Reference number: Z20933; MUID:99171579; PMID:10073571
A;Accession: T30916
A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA
A;Residues: 1-1446 <FAN>
A;Cross-references: UNIPROT:O77063; EMBL:AF007570; NID:g3642735; PID:g3642736; PIDN:AAC3.
C;Keywords: hydrolase; metallo-carboxypeptidase
Query Match 14.9%; Score 458.5; DB 2; Length 1446;
Best Local Similarity 38.1%; Pred. No. 4.3e-26;
Matches 96; Conservative 46; Mismatches 65; Indels 45; Gaps 6;
Qy 271 ILACPVSDDPNDL-----FLEAPASGSSDPLDFOHNYKAMKMLKMQVQPCNIT 320
Db 430 VTVVPGPEPDRMLMSYLDGLKDFSHHSSTHFKEPSEFVHNFMQMTKFLQDLADKYFALLA 489
Qy 321 RIYSGIKSYQGLKLYVMMSDKPGHELGEPVRYVAGMHGNEALGRELLLLMQFLCHE 380
Db 490 KLTSIQSGVQGRDLWLEITENFGQHPGKPEFKYIGNMHGNEVVVGRELLLLAQLLCEN 549
Qy 381 FLRGNPRVTRLLSEMRHLLPSMNPDPGYEIAHYHRSSE-LVGMAGRWNNQSIDLHNFAD 439
Db 550 YGQ-DDLVTLMLQQTRVHIMPSPNPDGYE---KREGDVSGIRGRANANLVDLNRNFPG 604
Qy 440 L--NTPLWEAQDDGKVPHVPNHHLPLPTYYTLPNATVAPETRAVIKMKRIPFVLSANL 497
Db 605 LFHTSVNERQE-----PETLAVMRWSRSLPFVLSANL 637
Qy 498 HGGELVVSYPPD 509
Db 638 HGGSLVANYPPD 649
RESULT 12
T13284
carboxypeptidase (EC 3.4.17.-) precursor - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
R;Settle, S.H.; Green, M.M.; Burtis, K.C.
Proc. Natl. Acad. Sci. U.S.A. 92, 9470-9474, 1995
A;Title: The silver gene of Drosophila melanogaster encodes multiple carboxypeptidases
A;Reference number: Z17649; MUID:96003800; PMID:7568156
A;Accession: T13284
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-1119 <SET>
A;Cross-references: EMBL:U29591; NID:g974552; PID:g974553; PIDN:AAA91650.1
C;Genetics: svr
A;Gene: svr
A;Cross-references: FlyBase:FBgn0004648
A;Map position: X
C;Keywords: hydrolase; metallo-carboxypeptidase
Query Match 14.3%; Score 439.5; DB 2; Length 1119;
Best Local Similarity 42.1%; Pred. No. 8.1e-25;
Matches 96; Conservative 31; Mismatches 68; Indels 33; Gaps 6;
Qy 284 LEAPASGSSDPLDFOHNYKAMKMLKMQVQPCNITRIYSGIKSYQGLKLYVMMSDKP 343
Db 441 LKKQFNGFLTPTKYEHNFNTAMESYLRATSSSYPSLTRLYSGIKSVQGRDLWLEIFATP 500
Qy 344 GEHELGEPEVRYVAGMHGNEALGRELLLLMQFLCHEFLRGN--PRVTRLLSEMRHLLPS 402
Db 501 GSHVPGVPPEKVVANMHGNEVVVGKELLILTKYMLERY--GNDDRITKLVNGTRMHFLYS 558
Qy 403 MNPDPGYEIAHYHRSSELVWGAEGRWNNSIDLHNFADLTPLEAQQDGKVPHVPNHHL 462
Db 559 MNPDPGYEISI-BGDRITGG--VGRANAHGIDLNRNFPD----- 592
Qy 463 PLPTYT-LPNATVAPETRAVIKMKRIPFVLSANLHGGLVSYPPD 509
Db 593 ---QYCTDRFNKTEPEVAAMVNTLSLDFVLSANLHGSLVANYPPD 637
RESULT 13

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OM protein - protein search, using sw model

Run on: January 10, 2005, 19:20:10 ; Search time 198 Seconds
(without alignment)

1668.005 Million cell updates/sec

Title: US-09-996-015-6

Perfect score: 3070

Sequence: 1 MWGLLLAALAPAVGPAALG.....GAKVPPDLRRRLRLRGQKD 574

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_02.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2975	96.9	734	2 Q6UW65	Q6UW65 homo sapien
2	2975	96.9	734	2 AAQ89315	AAQ89315 homo sapi
3	2974	96.9	734	2 Q6P4G8	Q6P4G8 homo sapien
4	2974	96.9	734	2 AAH63430	AAH63430 homo sapi
5	2972	96.8	734	1 CPXM_HUMAN	Q66sm3 homo sapien
6	2491	81.1	477	2 Q8N2E1	Q8N2E1 homo sapien
7	2378.5	77.5	722	1 CPXM_MOUSE	Q92l100 mus musculu
8	1400.5	45.6	764	1 CPX2_MOUSE	Q9d215 mus musculu
9	1390.5	45.3	756	1 CPX2_HUMAN	Q8n436 homo sapien
10	1357	44.2	430	2 Q8N2F1	Q8N2F1 homo sapien
11	1180.5	38.5	1128	2 Q88442	Q88442 mus musculu
12	1166	38.0	845	2 Q7KZ79	Q7KZ79 homo sapien
13	1166	38.0	1158	2 Q14113	Q14113 homo sapien
14	1166	38.0	1158	2 Q8IUX7	Q8IUX7 homo sapien
15	1073	35.0	728	2 Q97567	Q97567 bos taurus
16	1071.5	34.9	719	2 Q61281	Q61281 mus musculu
17	871	28.4	733	2 Q6ZSC7	Q6ZSC7 homo sapien
18	871	28.4	733	2 BAC87026	BAC87026 homo sapi
19	643.5	21.0	450	2 Q6NY94	Q6NY94 brachydanio
20	643.5	21.0	450	2 AAH66689	AAH66689 brachydan
21	628	20.5	652	2 O54858	O54858 rattus norv
22	628	20.5	652	2 O54859	O54859 rattus norv
23	624	20.3	654	2 Q8R4V4	Q8R4V4 mus musculu
24	616	20.1	458	1 CBPN_HUMAN	P15169 homo sapien
25	613.5	20.0	453	2 Q6PAY9	Q6PAY9 xenopus lae
26	613.5	20.0	453	2 AAH59995	AAH59995 xenopus l
27	609	19.8	641	2 O00520	O00520 homo sapien
28	604	19.7	457	2 Q9JUN5	Q9JUN5 mus musculu
29	604	19.7	458	2 Q91WM9	Q91WM9 mus musculu
30	599	19.5	457	2 Q9EQV8	Q9EQV8 rattus norv
31	582.5	19.0	454	1 CBPE_LOPAM	P37892 lophius ame

32	579	18.9	476	1 CBPE_RAT	P15087 rattus norv
33	574	18.7	476	1 CBPE_HUMAN	P16870 homo sapien
34	572	18.6	476	1 CBPE_MOUSE	Q00493 mus musculu
35	572	18.6	476	2 BAC33184	BAC33184 mus muscu
36	566	18.4	454	2 QGNSM5	Qnsm5 brachydanio
37	566	18.4	454	2 AAH70026	AAH70026 brachydan
38	562.5	18.3	434	1 CBPE_BOVIN	P04836 bos taurus
39	556.5	18.1	647	2 Q8QGP3	Q8qgp3 gallus gall
40	511.5	16.7	1380	2 Q86XE6	Q86xe6 homo sapien
41	506.5	16.5	1380	1 CBPD_HUMAN	O75976 homo sapien
42	506.5	16.5	1380	2 Q86SH9	Q86sh9 homo sapien
43	502	16.4	1377	1 CBPD_MOUSE	O89001 mus musculu
44	498.5	16.2	1133	2 Q9JHW1	Q9jhw1 rattus norv
45	498.5	16.2	1378	2 O35850	O35850 rattus norv

ALIGNMENTS

RESULT 1
Q6UW65 PRELIMINARY; PRT; 734 AA.
AC Q6UW65;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE CPXM.
GN ORFNames=UNQ3015;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,
Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
Godowski P.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
effort to identify novel human secreted and transmembrane proteins: a
bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
DR EMBL; AY358956; AAQ89315.1; -;
DR InterPro; IPR008969; CarboxypepD_reg.
DR InterPro; IPR000421; FA58 C.
DR InterPro; IPR008979; Gal_bind like.
DR InterPro; IPR000834; Peptidase_M14.
DR InterPro; IPR008575; Peptidase_M14B.
DR Pfam; PF00754; F5_F8 type C; 1.
DR Pfam; PF00246; Zn_carboxypept; 1.
DR PRINTS; PR00765; CBBOXYPEPTASE.
DR SMART; SM00231; FA58C; 1.
DR SMART; SM00631; Zn_pept; 1.
DR PROSITE; PS00132; CARBOXYPEPT_ZN_1; 1.
DR PROSITE; PS00133; CARBOXYPEPT_ZN_2; 1.
DR PROSITE; PS00133; CARBOXYPEPT_ZN_3; 1.
DR PROSITE; PS00222; FA58C_3; 1.
SQ SEQUENCE 734 AA; 81676 MW; B422FA5257301A38 CRC64;

Query Match 96.9%; Score 2975; DB 2; Length 734;
Best Local Similarity 78.1%; Pred.No. 6.1e-209;
Matches 573; Conservative 0; Mismatches 1; Indels 160; Gaps 1;

Qy	1	MWGLLLAALAPAVGPAALGAPNSVLGLAQPTTKVPGSTPALHSSPAQPPAETANGTS	60
Db	1	MWGLLLAALAPAVGPAALGAPNSVLGLAQPTTKVPGSTPALHSSPAQPPAETANGTS	60

Qy	61	BQVRIIRIVIKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTAGTLDPAEKQETGCPPLGL	120
Db	61	BQVRIIRIVIKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTAGTLDPAEKQETGCPPLGL	120
Qy	121	ESLVSOSRLEASSSOSFGLGPHRGRLNTOSGLEODLYDGAWCAEBQDADPWFQVDAGH	180
Db	121	ESLVSOSRLEASSSOSFGLGPHRGRLNTOSGLEODLYDGAWCAEBQDADPWFQVDAGH	180
Qy	181	PTPFGVITQGRNSVMRYDWVTYSKYQFSNDSTRTWGSRNHSSGMDAVFPANSDPETPVL	240
Db	181	PTPFGVITQGRNSVMRYDWVTYSKYQFSNDSTRTWGSRNHSSGMDAVFPANSDPETPVL	240
Qy	241	NLLEPEOVARFILLPQTLQGGAPCLRAEILLACVPSPNDLFLFAPASSGSDPLDFQHH	300
Db	241	NLLEPEOVARFILLPQTLQGGAPCLRAEILLACVPSPNDLFLFAPASSGSDPLDFQHH	300
Qy	301	NYKAMRKLKMQVOEQCFNTRIYSIGKSYQGLKLYVMEMSDKPGHEHGLGEPVRYVAGMH	360
Db	301	NYKAMRKLKMQVOEQCFNTRIYSIGKSYQGLKLYVMEMSDKPGHEHGLGEPVRYVAGMH	360
Qy	361	GNEALGRELLILLMQPLCFEPLRGHNPVTRLLSEMRIHLLPSMNPDCGYEIAYHRGSELVG	420
Db	361	GNEALGRELLILLMQPLCFEPLRGHNPVTRLLSEMRIHLLPSMNPDCGYEIAYHRGSELVG	420
Qy	421	WABGRWNNSIDLNHNFDADNPLWEAODDGKVHIVPNHHLLPLPTYTYTLPNATVAPETR	480
Db	421	WABGRWNNSIDLNHNFDADNPLWEAODDGKVHIVPNHHLLPLPTYTYTLPNATVAPETR	480
Qy	481	AVIKMKKRIPFVLSANLHGGLVVGYPDD-----	509
Db	481	AVIKMKKRIPFVLSANLHGGLVVGYPDD-----	509
Qy	510	-----	509
Db	541	LAMQDTSRRPCHSQDFS VHGNIINGADWHITVPGSMNDFS YLHNTCPVTVTVELSCDKFPH	600
Qy	510	-----	509
Db	601	NELPOEWENNKDALLTYLEQVRMGJAGVVRDKOTELGIADAVIADGINHDVTWTAMCGDY	660
Qy	510	-----MVTASAEGVHSTRNCRVTFEFGPPFCNFVLTKPKORRELLAAGAKVPP	560
Db	661	WRLLTPGDYMTVASAEGVHSTRNCRVTFEFGPPFCNFVLTKPKORRELLAAGAKVPP	720
Qy	561	DLRRRLERLRQKD 574	
Db	721	DLRRRLERLRQKD 734	
RESULT 2			
AAQ89315			
ID	AAQ89315	PRELIMINARY;	PRT; 734 AA.
AC	AAQ89315;		
DT	02-MAR-2004	(TremBLrel. 27, Created)	
DT	02-MAR-2004	(TremBLrel. 27, Last sequence update)	
DT	02-MAR-2004	(TremBLrel. 27, Last annotation update)	

RESULT	2
ID	AAQ89315
AC	PRELIMINARY; PRT;
AD	734 AA.
AT	AAQ89315
CT	(TREMBlrel. 27, Created)
DZ	02-MAR-2004
DT	02-NAR-2004 (TREMBlrel. 27, Last sequence update)
DT	02-WAR-2004 (TREMBlrel. 27, Last annotation update)
CPTM	.CPXM.
DE	UNQS015.
GK	Homo sapiens (Human).
OS	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC	Mammalia; Euarchia; Primata; Carnathini; Homnidae; Homo.
NCHI	TaxID=9606;
[1]	_RN
RN	SEQUENCE FROM N.A.
RP	PubMed=12575309;
RA	Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J., Chen J., Chow B., Choi C., Crowley C., Currell B., Deuel B., Dowd P., Eaton D., Foster J., Grimaldi C., Gu Q., Haas P.E., Heldens S., Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Lewis L., Lim D., Mark M., Robbie E., Sanchez C., Schoenfeld J., Seshagiri S., Simmons L., Singh J., Smith V., Stinson J. Vags A., Vandlen R., Watanabe C., Wiandt D., Woods K., Xie M.H., Yansura D., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,

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GN Name=CPXM;
OS Homo sapiens (Human) .
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RC SEQUENCE FROM N.A.
PC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RN SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR ENBL; BC063430; AAH63430.1;
DR GO; GO:0004180; F:carboxypeptidase activity; IEA.
DR InterPro; IPR008969; CarboxypepD_reg.
DR InterPro; IPR00421; FA58 C.
DR InterPro; IPR008979; Gal Bind like.
DR InterPro; IPR008834; Peptidase M14.
DR InterPro; IPR008575; Peptidase_M14B.
DR Pfam; PF05885; DUF857; 1.
DR Pfam; PF00754; F5_F8_type_C; 1.
DR Pfam; PF00246; Zn_carboxypept; 1.
DR PRINTS; PR00765; CRBOXYPTASEA.
DR SMART; SM00231; FA58C; 1.
DR SMART; SM00631; Zn_pept; 1.
DR PROSITE; PS00132; CARBOXYPEPT_ZN_1; 1.
DR PROSITE; PS00133; CARBOXYPEPT_ZN_2; 1.
DR PROSITE; PS50022; FA58C_3; 1.
DR Carboxypeptidase.
KW Carboxypeptidase.
SQ SEQUENCE 734 AA; 81693 MW; D5FFC614FE356102 CRC64;

Query Match 96.9%; Score 2974; DB 2; Length 734;
Best Local Similarity 78.1%; Pred. No. 7.2e-209;
Matches 573; Conservative 0; Mismatches 1; Indels 160; Gaps 1;

QY 1 MWGLLLAALAFAPAVGALCAPRNSVLGLAQPGTKKVGSTPALHSSPAQPPRAETANGTS 60
DB 1 MWGLLLAALAFAPAVGALCAPRNSVLGLAQPGTKKVGSTPALHSSPAQPPRAETANGTS 60
QY 61 EQHVRIRVIKKKVIKKRKKLLTRTPPLVTAGPLVTPPTAGTLPDAEKQETGCPPLGL 120
DB 61 EQHVRIRVIKKKVIKKRKKLLTRTPPLVTAGPLVTPPTAGTLPDAEKQETGCPPLGL 120
QY 121 ESLRVSLSRLAEASSQSGFLGPHRGLNLSQGLDGLYDGCWCAEEQDADPWFQVDAGH 180
DB 121 ESLRVSLSRLAEASSQSGFLGPHRGLNLSQGLDGLYDGCWCAEEQDADPWFQVDAGH 180
QY 181 PTFPSGVITGRNSVRWRYDWTYSKYQFNSDRTWGSNRHSSGMDAVFPANSDPTPVL 240
DB 181 PTFPSGVITGRNSVRWRYDWTYSKYQFNSDRTWGSNRHSSGMDAVFPANSDPTPVL 240
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RN      [2]
RP      SEQUENCE FROM N.A.
RC      TISSUB=Brain;
RA      Strauberg R.;
RL      Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR      EMBL; BC063430; AAH63430.1; -.
KW      Carboxypeptidase.
SQ      SEQUENCE 734 AA; 81693 MW; D5FFC614FE356102 CRC64;

Query Match          96.9%; Score 2974; DB 2; Length 734;
Best Local Similarity 78.1%; Pred. No. 7.2e-209;
Matches 573; Conservative 0; Mismatches 1; Indels 160; Gaps 1;

QY      1  MWGLLLAALAFAPAVGALGAPNSVLGLAQPGTKVPGSTPALHSSPAQPPAETANGTS 60
Db      1  MWGLLLAALAFAPAVGALGAPNSVLGLAQPGTKVPGSTPALHSSPAQPPAETANGTS 60
QY      61  EOHVRIRVIKKKVIKKRKKLLTRPTPLVTAGPLVTPPTAGTLDPAEKQETGCPPLGL 120
Db      61  EOHVRIRVIKKKVIKKRKKLLTRPTPLVTAGPLVTPPTAGTLDPAEKQETGCPPLGL 120
QY      121  ESLRVSLSRLAASSQSFGPLGPHRGRINTQSGLEDGLYDGAWCABEQADPWFQVDAGH 180
Db      121  ESLRVSLSRLAASSQSFGPLGPHRGRINTQSGLEDGLYDGAWCABEQADPWFQVDAGH 180
QY      181  PTRFSGVITQGRNSVWRVYDWTYSKYQFNSDSTWGSNRHSSGMDAVFPANSDPTPYL 240
Db      181  PTRFSGVITQGRNSVWRVYDWTYSKYQFNSDSTWGSNRHSSGMDAVFPANSDPTPYL 240
QY      241  NLLPEQVQVAFIRLLPQTLQGGAPCLRAEILACPVSDPNDLFLEAPASGSDPLDFQHH 300
Db      241  NLLPEQVQVAFIRLLPQTLQGGAPCLRAEILACPVSDPNDLFLEAPASGSDPLDFQHH 300
QY      301  NYKAMKLMKQVQEQCPNTRIYSIGSKYQGLKLYWMSDKPGEHELGEPEVRYVAGNH 360
Db      301  NYKAMKLMKQVQEQCPNTRIYSIGSKYQGLKLYWMSDKPGEHELGEPEVRYVAGNH 360
QY      361  GNEALGRELLLLMQFLCHEFLRGNPRVTRLLSEMRHLLPSMNPDPGYIAVHRGSELVG 420
Db      361  GNEALGRELLLLMQFLCHEFLRGNPRVTRLLSEMRHLLPSMNPDPGYIAVHRGSELVG 420
QY      421  WAEGRWNNQSIDLNNHFNADLNTPLWBAQDDGKVPHTVVPNHLLPLTPYTYLNPATVAPETR 480
Db      421  WAEGRWNNQSIDLNNHFNADLNTPLWBAQDDGKVPHTVVPNHLLPLTPYTYLNPATVAPETR 480
QY      481  AVIKMKRKIPFVLSANLHGELVVSYPFD----- 509
Db      481  AVIKMKRKIPFVLSANLHGELVVSYPFDTPDPAVFRWLSTVYAGSN 540
QY      510  ----- 509
Db      510  ----- 509
QY      541  LAMQDTSRRPCHSQDSFVHGNINGADWTVFGSMNDFSYLHNTCFEVTVELSCDKFPHE 600
Db      510  ----- 509
QY      601  NELPQWENNKDALLTYLQVRMGVAGVVRDXTDELGIADAVIADVGINHDVTTAWGDY 660
QY      510  -----WVTASRGYHSVTRNCRVTFEEGPPFCNCFVLTTPKQRLRELLAAGAKVPP 560
Db      661  WRLLTTPGDMYMTASRGYHSVTRNCRVTFEEGPPFCNCFVLTTPKQRLRELLAAGAKVPP 720
QY      561  DLRRRLRLRGQKD 574
Db      721  DLRRRLRLRGQKD 734

RESULT 5
CPXM HUMAN
ID CPXM HUMAN STANDARD; PRT; 734 AA.
AC Q96SN3; O9NUB5;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
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SEQUENCE FROM N.A. (ISOFORM 2).
 RP TISSUE=Embryonic brain;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins L.F., Jordan H., Moore T., Max S.I., Wang J., Heih F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young J.W., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Marra M.A.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [a].
 RP SPICE ISOFORM(S) THAT ARE POTENTIAL NMD TARGET(S).
 RX PubMed=14759258; DOI=10.1186/gb-2004-5-2-r8;
 RA Hillman R.T., Green R.E., Brenner S.E.;
 RT "An unappreciated role for RNA surveillance";
 CC Genome Biol. 5:RESEARCH008.1-RESEARCH008.16(2004).
 CC -1- FUNCTION: May be involved in cell-cell interactions. No
 CC carboxypeptidase activity was found yet (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=Q96SM3-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q96SM3-2; Sequence=VSP_000780, VSP_000781;
 CC Note=May be produced at very low levels due to a premature stop
 CC codon in the mRNA, leading to nonsense-mediated mRNA decay. No
 CC experimental confirmation available;
 CC -1- SIMILARITY: Belongs to peptidase family M14.
 CC -1- SIMILARITY: Contains 1 P5/8 type C domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use by non-profit institutions as long as its content is in no way
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AK027661; BAB55275.1; -;
 CC EMBL; AL035460; CAB82246.1; -;
 CC EMBL; BC032692; AAH32692.1; -;
 CC HSSP; Q90240; 1H8L.
 CC MEROPS; M14.015; -;
 CC Genes; HGNC.15771; CPXM.
 DR InterPro; IPR008969; CarboxypepD_reg.
 DR InterPro; IPR0040421; FA58_C.
 DR InterPro; IPR008979; Gal_bind_like.
 DR InterPro; IPR000834; Peptidase_M14.
 DR InterPro; IPR008575; Peptidase_M14B.
 DR Pfam; PF05885; DUF857; 1.
 DR Pfam; PF00754; P5_P8_type_C; 1.
 DR Pfam; PF00246; Zn_carboxypept; 1.
 DR PRINTS; PR00765; CRBOXYPTASEA.
 DR SMART; SM00231; FA58C; 1.
 DR SMART; SM00631; Zn_pept; 1.
 DR PROSITE; PS00132; CARBOXYPEPT_ZN_1; 1.
 DR PROSITE; PS00133; CARBOXYPEPT_ZN_2; 1.
 DR PROSITE; PS01285; FA58C_1; FALSE_NEG.
 DR PROSITE; PS01286; FA58C_2; FALSE_NEG.

DR PROSITE; PS50022; FA58C_3; 1.
 KW Alternative splicing; Carboxypeptidase; Glycoprotein; Hydrolase;
 KW Metalloprotease; Signal; Zinc.
 FT SIGNAL 1 20 Potential.
 FT CHAIN 21 734 Potential carboxypeptidase x.
 FT DOMAIN 113 274 P5/8 type C.
 FT DOMAIN 70 73 Poly-Lys.
 FT DOMAIN 369 373 Poly-Leu.
 FT METAL 360 360 Zinc (By similarity).
 FT METAL 363 363 Zinc (By similarity).
 FT METAL 498 498 Zinc (By similarity).
 FT ACT_SITE 591 591 Nucleophile (By similarity).
 FT DISULFID 115 274 By similarity.
 FT CARBOHYD 57 57 N-linked (GLCNAC. .) (Potential).
 FT CARBOHYD 210 210 N-linked (GLCNAC. .) (Potential).
 FT CARBOHYD 220 220 N-linked (GLCNAC. .) (Potential).
 FT CARBOHYD 318 318 N-linked (GLCNAC. .) (Potential).
 FT CARBOHYD 428 428 N-linked (GLCNAC. .) (Potential).
 FT CARBOHYD 472 472 N-linked (GLCNAC. .) (Potential).
 FT VARSPLIC 308 356 LMKQVQECPNITRIYSIGKSYQGLKLYNMESDKFGEHEL
 FT GEPEVRVY -> VRYNPYDILGRRAHPQSVPFPSPSHRGTTCC
 FT DCACMPLLPDVSFAFSVPDP (in isoform 2).
 FT /FTId=VSP_000780.
 FT Missing (in isoform 2).
 FT VARSPLIC 357 734 /FTId=VSP_000781.
 FT CONFLICT 390 390 W -> R (in Ref. 2).
 FT SEQUENCE 734 AA; 81697 MW; 815705578E8A58F3 CRC64;
 SQ
 Query Match 96.8%; Score 2972; DB 1; Length 734;
 Best Local Similarity 78.1%; Pred. No. 1e-208;
 Matches 573; Conservative 0; Mismatches 1; Indels 160; Gaps 1;
 QY 1 MWGLLLAALAAPAVGALCAPNSVLGLAQPGCTTKVPGSTPALHSSPAQPPAETANGTS 60
 DB 1 MWGLLLAALAAPAVGALCAPNSVLGLAQPGCTTKVPGSTPALHSSPAQPPAETANGTS 60
 QY 61 EQHVRIRVTKKKKVMKKRKKLTLRPTPLVTAGPLVTPPTAGTLPDAEKQETGCPPLGL 120
 DB 61 EQHVRIRVTKKKKVMKKRKKLTLRPTPLVTAGPLVTPPTAGTLPDAEKQETGCPPLGL 120
 QY 121 ESURVSDSRLEASSOSFGLGPHRGRLNTQSGLEDGLVDGAWCAEEQDADPFQVDAGH 180
 DB 121 ESURVSDSRLEASSOSFGLGPHRGRLNTQSGLEDGLVDGAWCAEEQDADPFQVDAGH 180
 QY 181 PTRFSGVITQGRNSVMRYDWVTSYKQFNSDRTWGSNRHSSGMDAVFPANSDPETPVL 240
 DB 181 PTRFSGVITQGRNSVMRYDWVTSYKQFNSDRTWGSNRHSSGMDAVFPANSDPETPVL 240
 QY 241 NLLPEQVARFIRLLPQTWLGQAPCLRAEILACPVSDPNDLFLFAPAGSSDPLDFQHH 300
 DB 241 NLLPEQVARFIRLLPQTWLGQAPCLRAEILACPVSDPNDLFLFAPAGSSDPLDFQHH 300
 QY 301 NYKAMRKLKMQVQEQCPNITRIYSIGKSYQGLKLYNMESDKFGEHELGEPEVRYVAGMH 360
 DB 301 NYKAMRKLKMQVQEQCPNITRIYSIGKSYQGLKLYNMESDKFGEHELGEPEVRYVAGMH 360
 QY 361 GNEALGRELLLLLMQFLCHEFLRGNGPRVTRLLSEMRHLLPSMNPQGYEYAYHRGSELVG 420
 DB 361 GNEALGRELLLLLMQFLCHEFLRGNGPRVTRLLSEMRHLLPSMNPQGYEYAYHRGSELVG 420
 QY 421 WAEGRWNNQSI DLNHNHFNADLNTPLWEAQDQGVPHIVPNHHLPLPTTYTLPNATVAPETR 480
 DB 421 WAEGRWNNQSI DLNHNHFNADLNTPLWEAQDQGVPHIVPNHHLPLPTTYTLPNATVAPETR 480
 QY 481 AVIKMKWKRI PFVL SANLHGGELVVSYPFD ----- 509
 DB 481 AVIKMKWKRI PFVL SANLHGGELVVSYPFD ----- 509
 QY 510 ----- 509
 DB 541 LAMQDTSRRPCHQSQDSVHGNTINGADWTWTPGSMNDFSYLHTNCFEVTVELSCDFPHE 600
 QY 510 ----- 509

Db	601	NELPQWENNKDALLTYL	EQVRMGVVRDKDTLGIADAVIAVDGINHDVTTAWGGDY	660
Qy	510	-----MYTASAGYHSVTRN	CRVTFEEGGFFPCNFVLTQKQRLRELLAAGAKVPP	560
Db	661	WRLTTPGDYMYTASAGYHSVTRN	CRVTFEEGGFFPCNFVLTQKQRLRELLAAGAKVPP	720
Qy	561	DLRRRLRLRGQKD	574	
Db	721	DLRRRLRLRGQKD	734	
RESULT 6				
Q8N2E1	PRELIMINARY; PRT; 477 AA.			
ID	Q8N2E1			
AC	Q8N2E1			
DT	01-OCT-2002	(TrEMBLrel. 22, Created)		
DT	01-OCT-2002	(TrEMBLrel. 22, Last sequence update)		
DT	01-OCT-2003	(TrEMBLrel. 25, Last annotation update)		
DE	Hypothetical protein P8EC0226.			
OS	Homo sapiens (human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Whole embryo;			
RA	Ota T., Nishikawa T., Suzuki Y., Kawai-Hio Y., Hayaashi K., Ishii S.,			
RA	Saito K., Yamamoto J., Wakamatsu A., Nagai T., Nakamura Y.,			
RA	Nagahari K., Sugano S., Isogai T.;			
R-	Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AK075527; BAC11672.1; -			
DR	HSSP; Q90240; 1HL8.			
DR	GO; GO:0004182; F:carboxypeptidase A activity; IEA.			
DR	GO; GO:0004180; F:carboxypeptidase activity; IEA.			
DR	GO; GO:0007155; P:cell adhesion; IEA.			
DR	GO; GO:0006508; P:proteolysis and peptidolysis; IEA.			
DR	InterPro; IPR000421; FA58 C.			
DR	InterPro; IPR008979; Gal Bind like.			
DR	InterPro; IPR000834; Peptidase M14.			
DR	Pfam; PF00754; F5_F8 type C; 1.			
DR	Pfam; PF00246; Zn_carboxypept; 1.			
DR	PRINTS; PR00765; CRBOXYPTASEA.			
DR	SMART; SM00231; FA58C; 1.			
DR	SMART; SM00631; Zn pept; 1.			
DR	PROSITE; PS00132; CARBOXYPEPT_ZN_1; 1.			
DR	PROSITE; PS50022; FA58C_3; 1.			
KW	Carboxypeptidase.			
SQ	SEQUENCE 477 AA; 52766 MW; 0A3FBE477B57A246 CRC64;			
Query Match				
Best Local Similarity 99.8%; DB 2; Length 477;				
Matches 464; Conservative 0; Mismatches 1; Indels 0; Gaps 0;				
Qy	1	MMGLLALAAAPAVGVPALGAPRNSVLGLAQGTGTTKVGSTPALHSSPAQPAETANGTS	60	
Db	1	MMGLLALAAAPAVGVPALGAPRNSVLGLAQGTGTTKVGSTPALHSSPAQPAETANGTS	60	
Qy	61	EQHVRIRVIRIKKKVIMKKRKLTLTRPTPLVTPAGLVTPTPAGTLDPAEKQETGCPPLGL	120	
Db	61	EQHVRIRVIRIKKKVIMKKRKLTLTRPTPLVTPAGLVTPTPAGTLDPAEKQETGCPPLGL	120	
Qy	121	ESLRVSDSLSSSSQSGFLGPHRGLNLTQSGLEDGLYDGAWCAEEDADPFWQVDAGH	180	
Db	121	ESLRVSDSLSSSSQSGFLGPHRGLNLTQSGLEDGLYDGAWCAEEDADPFWQVDAGH	180	
Qy	181	PTFRFGSVITQGRNSVWRVDWVTSYKQFSNDSTRWWSGRNHSNGMDAVFPANSDPETPVL	240	
Db	181	PTFRFGSVITQGRNSVWRVDWVTSYKQFSNDSTRWWSGRNHSNGMDAVFPANSDPETPVL	240	
Qy	241	NLLPPEQVARFIRLLPQTLQGGAPCLRAELIACPVSDPNDLFLFAPASGSSDPLDFQHH	300	
Db	241	NLLPPEQVARFIRLLPQTLQGGAPCLRAELIACPVSDPNDLFLFAPASGSSDPLDFQHH	300	

Qy	301	NYKAMKLMKQVQEQCPNITRIYSIGKSYQGLKLYVMEMSDKPGEHELGEPEVRYVAGMH	360
Db	301	NYKAMKLMKQVQEQCPNITRIYSIGKSYQGLKLYVMEMSDKPGEHELGEPEVRYVAGMH	360
Qy	361	GNEALGRELLLLLMQFLCHEFLRGNPRVTRLSEMRILLPSMNDPGVEIAYHRSSELVG	420
Db	361	GNEALGRELLLLLMQFLCHEFLRGNPRVTRLSEMRILLPSMNDPGVEIAYHRSSELVG	420
Qy	421	WAEGRWNQSIDLNNFADLNTPLWEAQDDGKVPHIYVNHHLPLP	465
Db	421	WAEGRWNQSIDLNNFADLNTPLWEAQDDGKVPHIYVNHHLPLP	465
RESULT 7			
CPXM_MOUSE			
ID	CPXM_MOUSE	STANDARD; PRT; 722 AA.	
AC	Q9Z100; Q99LA3;		
DT	28-FEB-2003	(Rel. 41, Created)	
DT	28-FEB-2003	(Rel. 41, Last sequence update)	
DT	05-JUL-2004	(Rel. 44, Last annotation update)	
DE	Potential carboxypeptidase X precursor (EC 3.4.17.-)		
DE	(Metalloprotein carboxypeptidase CPX-1).		
GN	Name=Cpxm; Synonyms=Cpxm1, Cpx1;		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
[1]	SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND DEVELOPMENTAL STAGE.		
RN	TISSUE=Heart;		
RC	MEDLINE=99171585; PubMed=10073577;		
RX	Lei Y., Xin X., Morgan D., Pintar J.E., Fricker L.D.;		
RA	Identification of mouse CPX-1, a novel member of the		
RT	metalloprotein carboxypeptidase gene family with highest similarity to CPX-		
RT	2."		
RL	DNA Cell Biol. 18:175-185(1999).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Breast tumor;		
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;		
RA	Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,		
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,		
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,		
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,		
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,		
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,		
RA	Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,		
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,		
RA	Boeak S.A., McSwain P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,		
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,		
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,		
RA	Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,		
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,		
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,		
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,		
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,		
RA	Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.;		
RT	Generation and initial analysis of more than 15,000 full-length human		
RT	and mouse cDNA sequences."		
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).		
CC	-/- FUNCTION: May be involved in cell-cell interactions. No		
CC	carboxypeptidase activity was found yet.		
CC	-/- SUBCELLULAR LOCATION: Secreted (Probable).		
CC	-/- TISSUE SPECIFICITY: Strongly expressed in testis and spleen.		
CC	Moderately expressed in salivary gland, brain, heart, lung, and		
CC	kidney. Extremely low expression in liver and muscle. No		
CC	expression in eye, adrenal, and white adipose tissues.		
CC	-/- DEVELOPMENTAL STAGE: First expressed at 13.5 dpc, in the meninges,		
CC	nasal mesenchyme, primordial cartilage and skeletal structures.		
CC	-/- SIMILARITY: Belongs to peptidase family M14.		
CC	-/- SIMILARITY: Contains 1 F5/8 type C domain.		

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CC DR EMBL; AF077738; AAD15985.1; -
 CC DR EMBL; BC003713; AAH03713.1; -
 CC DR HSSP; O90240; 1H8L.
 CC DR MEROPS; M14.015; -
 CC DR MGD; MGI:1934569; Cpxm1.
 CC DR GO; GO:0005615; C:extracellular space; IDA.
 CC DR InterPro; IPR008969; Carboxypepd_reg.
 CC DR InterPro; IPR00421; FA58_C.
 CC DR InterPro; IPR008979; Gal_bind_like.
 CC DR InterPro; IPR008834; Peptidase_M14.
 CC DR InterPro; IPR008575; Peptidase_M14B.
 CC DR Pfam; PF05885; DUF857; 1.
 CC DR Pfam; PF00754; F5_F8_type_C; 1.
 CC DR Pfam; PF00246; Zn_carboxypept; 1.
 CC DR PRINTS; PR00765; CRBOXYPTASEA.
 CC DR SMART; SM00231; FA58C; 1.
 CC DR SMART; SM00631; Zn_pept; 1.
 CC DR PROSITE; PS00132; CARBOXYPEPT_ZN_1; 1.
 CC DR PROSITE; PS00133; CARBOXYPEPT_ZN_2; 1.
 CC DR PROSITE; PS01285; FA58C_1; 1.
 CC DR PROSITE; PS01285; FA58C_2; FALSE_NEG.
 CC DR PROSITE; PS00222; FA58C_3; 1.
 CC DR Carboxypeptidase; Glycoprotein; Hydrolase; Metalloprotease; Signal;
 CC DR Zinc.
 CC FT SIGNAL 1 20 Potential.
 CC FT CHAIN 21 722 Potential carboxypeptidase X.
 CC FT DOMAIN 103 263 F5/8 type C.
 CC FT DOMAIN 62 65 Poly-Lys.
 CC FT DOMAIN 358 362 Poly-Leu.
 CC FT METAL 349 349 Zinc (By similarity).
 CC FT METAL 352 352 Zinc (By similarity).
 CC FT METAL 487 487 Zinc (By similarity).
 CC FT ACT_SITE 580 580 Nucleophile (By similarity).
 CC FT DISULFID 105 263 By similarity.
 CC FT CARBOHYD 49 49 N-linked (GlcNAc...) (Potential).
 CC FT CARBOHYD 200 200 N-linked (GlcNAc...) (Potential).
 CC FT CARBOHYD 210 210 N-linked (GlcNAc...) (Potential).
 CC FT CARBOHYD 307 307 N-linked (GlcNAc...) (Potential).
 CC FT CARBOHYD 461 461 N-linked (GlcNAc...) (Potential).
 CC FT CONFLICT 253 253 V -> A (in Ref. 2).
 CC SQ SEQUENCE 722 AA; 80934 MW; 2A0B59A7A92142BF CRC64;
 Query Match 77.5%; Score 2378.5; DB 1; Length 722;
 Best Local Similarity 64.3%; Pred. No. 2.7e-165;
 Matches 471; Conservative 34; Mismatches 57; Indels 171; Gaps 5;
 QY 1 MWGLLLAALAPAVGALGAPNSVLGLAQPGTKKPGSTPALHSSPAQPPAETANGTS 60
 DB 1 MWGLLLAVTAFAPSVGLIGLAPSAVPEGLA-----PGSTLAPHSSVAQPSIK-ANETS 52
 QY 61 EQHVRIRVIKKKVIKKRKKLLTRTPPLVTAGPLVTPPTAGTLDPAEKQETGCPPLGL 120
 DB 53 ERHVRIRVIKKKVIKKRKK--LRHEGPIGTARPVVPTHPAKTLTLPEKQEPGLGL 110
 QY 121 ESRVSDSRLEASSQSFGHGHRGRNLINOSGLEDGLYDGACAEQDADPWFQVDAGH 180
 DB 111 ESRVSDSRLEASSQSFGHGHRGRNLINOSGLEDGLYDGACAEQDADPWFQVDAGH 170
 QY 181 PTFSGVITQGRNSVMRYDVTYKVFNSDRTWGRNSHSSGMDVFPANSDPTFVL 240
 DB 171 PVFAGVITQGRNSVMRYDVTYKVFNSDRTWGRNSHSSGMDVFPANSDPTFVL 229
 QY 241 NLLPEQVAFIRLLPOTWLGGAAPCLRAEILACPVSDPNDLFLFAPAGSSDPLDFQHH 300
 DB 230 NLLPEQVAFIRLLPOTWLGGAAPCLRAEILACPVSDPNDLFLFAPAGSSDPLDFRHH 289

QY 301 NYKAMRKLKQVOQCNPNTIRIYSIGKSYOGLKLYVMEMSDKPCHEHLGPEVRYVAGMH 360
 DB 290 NYKAMRKLKQVOQCNPNTIRIYSIGKSHOGLKLYVMEMSDHPCHEHLGPEVRYVAGMH 349
 QY 361 GNEALGRELHLLLMQFLCHEFLRGNPRVTRLLSEMR IHLPLSPMNPDCGYEYAYHRGSELVG 420
 DB 350 GNEALGRELHLLLMQFLCHEFLRGNPRVTRLLSEMR IHLPLSPMNPDCGYEYAYHRGSELVG 409
 QY 421 WAEGRWNNOSIDLNHNFPADLNTPLWEAQDDGKVPHTVNPVHHLPLPTYYTLPNATVAPETR 480
 DB 410 WAEGRWTHQGDIDLNHNFPADLNTQLWAEDDGLVPTVNPVHHLPLPTYYTLPNATVAPETR 469
 QY 481 AVIKWKKRIFPVLNHLGELVVSYPFDM----- 510
 DB 470 AVIKWKKRIFPVLNHLGELVVSYPFDM----- 509
 QY 511 ----- 510
 DB 530 RAMQDTRRRPCHSQDFSLHGNVINGADWHTVPGSMNDFSYLHTNCFEVTVELSCDKPPHE 589
 QY 511 ----- 510
 DB 590 KELPQEWNNKDALLTYLEQVRMGITGVVRDKDTGLGIADAVIAVEGINHDVTTAWGGDY 649
 QY 511 -----VTASAEGYHSVTRNCRVTFEGFPFCNVLTKPKQRLRELLAAGAKVPP 560
 DB 650 WRLLTPGDYVVTASAEGYHVRQHCQVTFEGFPVCNVLTKPKQRLRELLAATRGKLP 709
 QY 561 DLRRRLRLRGOK 573
 DB 710 DLRRRLRLRGOK 722
 RESULT 8
 ID CPX2 MOUSE STANDARD; PRT; 764 AA.
 AC Q9D2L5; O54860; Q8VDQ4;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Potential carboxypeptidase-like protein X2 precursor.
 GN Name=Cpxm2; Synonyms=Cpx2;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
 RC TISSUE=Heart, and Kidney;
 RX MEDLINE=99025623; PubMed=9809751;
 RA Xin X., Day R., Dong W., Lei Y., Fricker L.D.;
 RT "Identification of mouse CPX-2, a novel member of the
 RT metalcarboxypeptidase gene family: cDNA cloning, mRNA distribution,
 RT and protein expression and characterization.";
 RL DNA Cell Biol. 17:897-909(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Skin;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Quackenbush J.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt J., Brusic V., Chothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,

Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S., Ravasi T., Reed D.J., Reid J., Ring B.Z., Ringwald M., Sandelin A., Schneider C., Sempie C.A., Setou M., Shimada K., Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M., Verardo R., Wagner L., Wallestedt C., Wang Y., Watanabe Y., Wells C., Wilming L.G., Wynshaw-Boris A., Yangisawa M., Yang I., Yang L., Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N., Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Shiraki T., Waki K., Kawai J., Mizawa K., Arakawa T., Fukuda S., Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney E., Hayaishizaki Y., Nature 420:563-573(2002).

"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs"; Nature 420:563-573(2002).

SEQUENCE FROM N.A.

TISSUE=Breast tumor;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L.H., Shenmen C.M., Schuler G.D., Atschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J., Boeak S.A., McWen P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahy J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

- FUNCTION: May be involved in cell-cell interactions.

- SUBCELLULAR LOCATION: Secreted (Probable).

- TISSUE SPECIFICITY: Highly expressed in lung and kidney. Moderate expression in liver and brain, including the cerebral cortex, piriform cortex, nucleus of the lateral olfactory tract, hippocampus, habenular nucleus and choroid plexus.

- SIMILARITY: Belongs to peptidase family M14.

- SIMILARITY: Contains 1 F5/8 type C domain.

- CAUTION: As it has lost active sites residues and zinc-binding sites it is unlikely to be catalytically active.

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EMBL; AF017639; AAC04670.1; -

EMBL; AK019509; BAB31768.1; -

EMBL; BC021444; AAH21444.1; -

HSSP; Q90240; 1H8L.

MEROPS; M14.019; -

MGD; MGI:1926006; Cpm2.

InterPro; IPR008969; Carboxypeptid_reg.

InterPro; IPR000421; F5/8 C.

InterPro; IPR008979; Gal_Bind_like.

InterPro; IPR000834; Peptidase_M14.

InterPro; IPR008575; Peptidase_M14B.

Pfam; PF05885; DUF857; 1.

Pfam; PF00754; F5_F8 type C; 1.

Pfam; PF00246; Zn_Carboxypept; 1.

PRINTS; PR00765; CRBOXYPTASEA.
SMART; SM00231; FAS8C; 1.
SMART; SM00631; Zn_pept; 1.
PROSITE; PS00132; CARBOXYPEPT_ZN_1; 1.
PROSITE; PS01285; FAS8C_1; 1.
PROSITE; PS01286; FAS8C_2; 1.
PROSITE; PS00022; FAS8C_3; 1.
KW Glycoprotein; Signal.
FT SIGNAL 1 27
FT CHAIN 28 764
FT DOMAIN 142 301
FT FT F5/8 type C.
FT POLY-LEU.
FT DISULFID 144 301
FT CARBOHYD 239 239
FT CARBOHYD 249 249
FT CARBOHYD 289 289
FT CARBOHYD 345 345
FT CARBOHYD 499 499
FT CONFLICT 49 49
FT CONFLICT 58 58
FT CONFLICT 65 65
FT CONFLICT 402 402
FT CONFLICT 409 409
FT CONFLICT 469 469
SQ SEQUENCE 764 AA; 86963 MW; 2813CBEE0C5A149A CRC64;

Query Match 45.6%; Score 1400.5; DB 1; Length 764;
Best Local Similarity 39.6%; Pred. No. 1.1e-93;
Matches 302; Conservative 78; Mismatches 176; Indels 207; Gaps 10;

QY 4 LLLAALAPAV-----GPALGAP-----RNSVLGLAQTGTTKVGSTPALH--- 45
Db 11 LALLALVALAGVRAAGAAFEEDYYSQELMRGRYYGHPEPEPEQELFS-PSMHDL 69
QY 46 ---SSPAQPPAETANGTSEQHVIRVIVKKKVIKKKKLTLTRTP----- 89
Db 70 RVESEQEQEPHQGHRTPK-----KAIKPKA--PKEKLVAETPPPKNSNRGRSKN 122
QY 90 LVTAGPLVTPPTAGTLPDAEKQETGCPPLGLSIRVSDSRLEASSQSFGIGHGRINI 149
Db 123 LEKAASDDHGVPVAHEDVRE---SCPLGLETLKITDFQLHASTSKRYGLGAHGRINI 178
QY 150 QSGLEDGLYDGAWCAEQADPMFOVDAGHPTFSGVITQGRNSVVRVYDWVTSYKQFS 209
Db 179 QAGINENDFYDGAACGRNDLHQWIEVDARLTKFTGVTQGRNSLWLSMDVTSYKQVWS 238
QY 210 NDSRTWGRNSHSSGMDAVFPANSDPETPVNLPLPEQVAFIRLLPQTWLOGGAPCLRA 269
Db 239 NDSHTWTVKNGSG--DMIFEGNSEKEIPVLNLPVPMVARYINPQSMFDNGSICWRM 296
QY 270 EILACPVSDPNDLPLEAPAGSSDPLDFQHNHYKAMKLMKQVQEQCPNTRIYSIKSY 329
Db 297 EILGCPPLDPNNYHRRNEMTTDDLDLFKHNYKEMRQLMKVNMCPNTRIYNIKSH 356
QY 330 QGLKLYWMSDKPGEHELGEPEVRYVAGHMGNEALGRELLLMQLFCHFLAGNPRVT 389
Db 357 QGLKLYAVEISDRPGEHEVEGEPEPHYTAGHNEVLGRELLLLHLFLQEYSQANRIV 416
QY 390 RLLESEMRHLLPSMNPDPGYEIAHRGSELVGVAGRWNNQSIDLNHNFADINTPLWEAQD 449
Db 417 RLVEETRIHILPSLNPDPGYEKAVEGSGELSGWSLGRWTHDGDINNFPDLNLSLWEAD 476
QY 450 DGKVPVHPNHHPLPYTYTLPLNATVAPETRAVIMKMKRIIPFVLSANLHGGELVVSYPFD 509
Db 477 QONAPRKVPNHYIAIPFWFLSENAITVATETRAVIAMMEKIIPFVLGGNLOGGELVWAYPYD 536
QY 510 M----- 510
Db 537 MVRSMLKTOEHTPTPDHVRFLWLAYSASTHRLMTDARRRVCHTEDFQKEEGTVNGASWH 596
QY 511 ----- 510

Db 597 TVAGSLNDFSYLHNTNCFELSIYVCDKYPHSELPPEWNNRSLIVFMQVHRGIKIV 656
 Qy 511 -----VTASAGYHVSVTRNCRVTFE 530
 Db 657 RDLOGKGISNAVISVEGVNHDIRTSADGDYWRLLNPGYVVTAKAGFTSTKCMWGYD 716
 Qy 531 EGPFPNVLTKTPKQRLRELLAAGAKVPPDRLRLRLRQOK 573
 Db 717 MGATRCDFTLTKNLARIREIMETFGKQVSLPSRLKLRGRK 759

RESULT 9
 CPX2 HUMAN STANDARD; PRT; 756 AA.
 AC Q8N436;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUN-2004 (Rel. 44, Last annotation update)
 DE Potential carboxypeptidase-like protein X2 precursor (UNQ676/PRO1310).
 GN Name=CPXM2;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
 RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
 RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
 RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
 RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
 RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
 RA Seshagiri S., Simmons C., Singh J., Smith V., Stinson J., Vagts A.,
 RA Vandlen R., Watanabe C., Wiedand D., Woods K., Xie M.-H., Yansura D.,
 RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
 RA Godowski P., Gray A.;
 RA "The secreted protein discovery initiative (SPDI), a large-scale
 RT effort to identify novel human secreted and transmembrane proteins: a
 RT bioinformatics assessment.";
 RL Genome Res. 13:2265-2270(2003).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain, and Lung;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Straube R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Boak S.A., McEwan K.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: May be involved in cell-cell interactions.
 CC -!- SUBCELLULAR LOCATION: Secreted (Probable).
 CC -!- SIMILARITY: Belongs to peptidase family M14.
 CC -!- SIMILARITY: Contains 1 F5/8 type C domain.
 CC -!- CAUTION: As it has lost active sites residues and zinc-binding
 CC sites it is unlikely to be catalytically active.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation

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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AY358565; AAQ8928.1; .
 DR EMBL; BC036789; AAH36789.1; ALT_INIT.
 DR HSP; O90240; I48L.
 DR MEROPS; M14.019; .
 DR InterPro; IPR008969; CarboxypepD_reg.
 DR InterPro; IPR000421; F5/8 type C.
 DR InterPro; IPR008979; Gal_bind like.
 DR InterPro; IPR000834; Peptidase_M14.
 DR InterPro; IPR008575; Peptidase_M14B.
 DR Pfam; PF05885; DUF857; 1.
 DR Pfam; PF00754; F5_F8_type_C; 1.
 DR Pfam; PF00246; Zn_carboxypept; 1.
 DR PRINTS; PR00765; CRBOXYPTASEA.
 DR SMART; SM00231; FAS8C; 1.
 DR SMART; SM00631; Zn_pept; 1.
 DR PROSITE; PS00132; CARBOXYPEPT_ZN_1; 1.
 DR PROSITE; PS01285; FAS8C_1; 1.
 DR PROSITE; PS01286; FAS8C_2; 1.
 DR PROSITE; PS50022; FAS8C_3; 1.
 DR Glycoprotein; Signal.
 FT SIGNAL 1 25 Potential
 FT CHAIN 26 756 Potential carboxypeptidase-like protein
 FT X2,
 FT DOMAIN 134 293 F5/8 type C.
 FT DOMAIN 45 101 Pro-rich.
 FT DISULFID 136 293 Poly-Leu.
 FT CARBOHYD 231 231 By similarity.
 FT CARBOHYD 241 241 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 281 281 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 337 337 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 491 491 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 756 AA; 85897 MW; 1A2F1A5BA7C1D56E CRC64;
 Query Match 45.3%; Score 1390.5; DB 1; Length 756;
 Best Local Similarity 40.0%; Pred. No. 6.1e-93;
 Matches 299; Conservative 76; Mismatches 185; Indels 187; Gaps 8;
 Qy 4 LLLAALAPAVGALGAP-----RNSVLGLAQPGTKVPGSTPALHSSPAQPAE 54
 Db 15 LLAVTLAVGAAQAALDDPDYQETWSREPYARPEP---ELETSPPL---PAGEEE 68
 Qy 55 TANGTSEQHVRIRVIKKKVIKKKLTILTRPTPLVLTAGPLVTPT----PAGTLDPA-- 108
 Db 69 WERRPOEPRPPKEATPKKA--PKREKSAPEPPPGKHSNKKVMRTKSEKAANDHSVR 126
 Qy 109 ---EKQETGCPPLGLSRLSVSRRLSEASSQSFGLGPHGRGLNIQSGLEDGLYDGAWCA 165
 Db 127 VAREDVRESCPPLGLETLKITDQFLHASTVKRYGLGHRGLNIQAGINENDFYDGAWCA 186
 Qy 166 EEOADPMQVDAGHTRFSGVITQGRNSVWRVDMWTSYKVFQFNSDRTWGSRNHSSGM 225
 Db 187 GRNDLQOMLEVDAARRLTRITGVITQGRNSLWLSMDWTSYKVMVNSDHTVTVTKNGSG-- 244
 Qy 226 DAVFPANSDPETPVLNLLPEQVAREIRLLPOTWLOGGAPCLRAETILACVSPDNLDFLE 285
 Db 245 DMIFEGNSEKEIPVLNELPVPVARYIRINQSFNDSICMEWEILGCLPDPNNYHR 304
 Qy 286 APASGSSDPLDFOHNYKAMKLMQVQGCQPNITRIYSIGKSYQGLKLYVMSEMSKPGE 345
 Db 305 RNEMTTDDLDLFKHNYKEMRQLMKVVMNEMCPNITRIYNIGKSHQGLKLYAVEISHPGE 364
 Qy 346 HELGEPEVRYVAGMHCNEALGRELILLMQFLCHEFLGCPNPRVTRLLSEMRHLLPSMP 405
 Db 365 HEVGEPEFYIAGAHGNEVILGRELILLVQFVQCYELARNARIVHLVETRIHVLPSLNP 424
 Qy 406 DGVEIAYHRGSELVGAEGRWNNQSIDLNNHFNADLTPLWEAQDDGCKVPHIVPNHPLP 465

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Db 425 DGEKAYEGGSELGWSLGRWTHGIDINNFPDLNLLWEADRQVPRKVNHYIAIP 484
QY 466 TYTLPNATVAPETRAVIAKMKRIPFVLSANLHGELVSVYFDM----- 510
Db 485 EWFLSENATVAETRAVIAWMEKIPFVLGGNLQGGELVWVAYPYDLVRS PKTQEHPTPD 544
QY 511 ----- 510
Db 545 DHVFRWLAYSASTHRLMTDARRRCHTEDFQKEEGTVNGASWHTVAGSLNDFSYLHTNC 604
QY 511 ----- 510
Db 605 FELSIYVCDKYPHESQLPEWENNRESLIVFMEQVHRGIKGLVRDASHGKIPNIIISVE 664
QY 511 -----VTASAGYHSVTRNCRVTFEEGPFPCNFVLTPTKPKQ 546
Db 665 GINHDIRTANDGQYWRLLNFGYVVTAKAGFTASTKNCMVGYDMGATRCDFTLSTNMA 724
QY 547 RLRELLAAGAKVPPDLRRRLRLRGOK 573
Db 725 RIREIMEKFGQVSLPARLKLGRK 751
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RESULT 10

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Q8N2F1 ID Q8N2F1 PRELIMINARY; PRT; 430 AA.
AC Q8N2F1;
DT 01-OCT-2002 (TremBLrel. 22, Created)
DT 01-OCT-2002 (TremBLrel. 22, Last sequence update)
DE Hypothetical protein PSEC0206.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP TISSUE=Whole embryo;
RC SEQUENCE FROM N.A.
RA Ota T., Nishikawa T., Suzuki Y., Kawai-Hio Y., Hayashi K., Ishii S.,
RA Saito K., Yamamoto J., Wakanatsu A., Nagai T., Nakamura Y.,
RA Nagahari K., Sugano S., Isozaki T.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK075508; BAC11661.1; -.
DR HSSP; Q90240; 1H8L.
DR GO; GO:0004182; F:carboxypeptidase A activity; IEA.
DR GO; GO:0004183; F:carboxypeptidase E activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0005508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR008969; Carboxypeptid_reg.
DR InterPro; IPR008834; Peptidase_M14.
DR Pfam; PF05885; DUF857; 1.
DR Pfam; PF00246; Zn_carboxypept_1.
DR PRINTS; PR00765; CRBOXYPTASEA.
DR SMART; SM00631; Zn_pept; 1.
DR PROSITE; PS00132; CARBOXYPEPT_ZN_1; 1.
DR PROSITE; PS00133; CARBOXYPEPT_ZN_2; 1.
KW Carboxypeptidase.
SQ SEQUENCE 430 AA; 48905 MW; B4A3EDF3035FA34C CRC64;
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Query Match 44.2%; Score 1357; DB 2; Length 430;
Best Local Similarity 62.8%; Pred. No. 7,9e-91;
Matches 270; Conservative 0; Mismatches 0; Indels 160; Gaps 1;
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QY 305 MRKLMKQVQPCPNTRIYSIGKSYQGLKLYWEMSDRPGHELGEPEVRVYVAGHGNSEA 364
Db 1 MRKLMKQVQPCPNTRIYSIGKSYQGLKLYWEMSDRPGHELGEPEVRVYVAGHGNSEA 60
QY 365 LGRELLLLLMQFLCHEFLRGNPRVTRLISEMRIHLPLSPNPDGYEIAVHRGSELVGNWAG 424
Db 61 LGRELLLLLMQFLCHEFLRGNPRVTRLISEMRIHLPLSPNPDGYEIAVHRGSELVGNWAG 120
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QY 425 RWNOSIDLNNHNFADLNTPLWEAQDQGVPHIVPNHHLPLPTTYTLPNATVAPETRAVIK 484
Db 121 RWNOSIDLNNHNFADLNTPLWEAQDQGVPHIVPNHHLPLPTTYTLPNATVAPETRAVIK 180
QY 485 WNKRIPIPFVLSANLHGELVSVYFDP----- 509
Db 181 WNKRIPIPFVLSANLHGELVSVYFDPMTPTMAARELTPTPDDAVFRWLSTVYVAGSLNLAQ 240
QY 510 ----- 509
Db 241 DTSRRPCHSQDSFVHGNIINGADWHTVPGSMNDFSYLHTNCFEVTVELSCDKFPHENELP 300
QY 510 ----- 509
Db 301 QEWENKDALTYLEQVRMGIAGVVRDKDTGLGIADAVIADGINHDVTTAWGGSDYWRLL 360
QY 510 -----MVTASAGYHSVTRNCRVTFEEGPFPCNFVLTPTKPKORLELLAAGAKVPPDLRR 564
Db 361 TPGDYVMTASAGYHSVTRNCRVTFEEGPFPCNFVLTPTKPKORLELLAAGAKVPPDLRR 420
QY 565 RLRLRGOKD 574
Db 421 RLRLRGOKD 430
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RESULT 11

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Q88442 ID Q88442 PRELIMINARY; PRT; 1128 AA.
AC Q88442;
DT 01-NOV-1998 (TremBLrel. 08, Created)
DT 01-NOV-1998 (TremBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TremBLrel. 26, Last annotation update)
DE Aortic carboxypeptidase-like protein ACLP.
GN Name=Aebp1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=98288305; PubMed=9624159;
RA Layne M.D., Endege W.O., Jain M.K., Yet S.F., Hsieh C.M., Chin M.T.,
RA Perrella M.A., Blamir M.A., Haber E., Lee M.E.;
RT "Aortic carboxypeptidase-like protein, a novel protein with discoidin
RT and carboxypeptidase-like domains, is up-regulated during vascular
RT smooth muscle cell differentiation.";
RL J. Biol. Chem. 273:15654-15660(1998).
DR EMBL; AF053943; AAC25584.1; -.
DR HSSP; Q90240; 1H8L.
DR MEROPS; M14.951; -.
DR MGD; MGI:1197012; Aebp1.
DR GO; GO:0004180; F:carboxypeptidase activity; IEA.
DR GO; GO:0003714; F:transcription corepressor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000421; FA58_C.
DR InterPro; IPR008979; Gal_bind_like.
DR InterPro; IPR000834; Peptidase_M14.
DR InterPro; IPR008575; Peptidase_M14B.
DR Pfam; PF05885; DUF857; 1.
DR Pfam; PF00754; F5_F8_type_C; 1.
DR Pfam; PF00246; Zn_carboxypept_1.
DR PRINTS; PR00765; CRBOXYPTASEA.
DR SMART; SM00231; FAS8C; 1.
DR SMART; SM00631; Zn_pept; 1.
DR PROSITE; PS00132; CARBOXYPEPT_ZN_1; 1.
DR PROSITE; PS01285; FAS8C_1; 1.
DR PROSITE; PS01286; FAS8C_2; UNKNOWN_1.
DR PROSITE; PS00022; FAS8C_3; 1.
KW Carboxypeptidase.
SQ SEQUENCE 1128 AA; 128265 MW; 834F46A892CC5CD5 CRC64;
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Query Match 38.5%; Score 1180.5; DB 2; Length 1128;
Best Local Similarity 37.8%; Pred. No. 2.5e-77;
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QY	511	-----	510
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Db	792	ARGDEDEVSEAEQTPDHAIFRWLAISFASAHLLTLTPYRGCGQAQDYTGGMGIUNGAKW	851
QY	511	-----	510
Db	852	NPRTGTINDFSYLHTNCLLSFYLGCDFPFHESELPREWENNKALLTFMEQVHRGKGV	911
QY	511	-----	510
Db	912	VTDSQGPPIANATISVSGINHGKVTASGGDYWILLNPGEVTVTAHAEGYTPSAKTCNV	971
QY	530	EEGPFPCNFVLTQPKQRLRELJAAGAKVP-----PDLR-----RLRL-----RLRG	571
Db	972	DIGATQCNFILARSNWKRIEIMANGNRDIPHDPSRPMTPQORRLQORRLRLRLRA	1031
QY	572	Q 572	
Db	1032	Q 1032	
RESULT 14			
QY	810X7	PRELIMINARY; PRT; 1158 AA.	
Db	810X7		
QY	01-MAR-2003	(TREMELrel. 23, Created)	
Db	01-MAR-2003	(TREMELrel. 23, Last sequence update)	
QY	01-MAR-2004	(TREMELrel. 26, Last annotation update)	
Db	01-MAR-2004	(TREMELrel. 26, Last annotation update)	
QY	Adipocyte	enhancer binding protein 1,.	
Db	Adipocyte	enhancer binding protein 1,.	
QY	Name=ABEP1		
Db	Name=ABEP1		
QY	Homo sapiens	(Human).	
Db	Homo sapiens	(Human).	
QY	Eukaryota; Metazoa;	Chordata; Craniata; Vertebrata; Euteleostomi;	
Db	Eukaryota; Metazoa;	Chordata; Craniata; Vertebrata; Euteleostomi;	
QY	Mammalia; Eutheria;	Primates; Catarrhini; Hominiidae; Homo.	
Db	Mammalia; Eutheria;	Primates; Catarrhini; Hominiidae; Homo.	
QY	NCBI_TaxID=9606;		
Db	NCBI_TaxID=9606;		
QY	SEQUENCE FROM N.A.		
Db	SEQUENCE FROM N.A.		
QY	TISSUE=Brain;		
Db	TISSUE=Brain;		
QY	MEDLINE=22388257;	PubMed=12477932;	
Db	MEDLINE=22388257;	PubMed=12477932;	
QY	Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,		
Db	Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,		
QY	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,		
Db	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,		
QY	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,		
Db	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,		
QY	Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,		
Db	Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,		
QY	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,		
Db	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,		
QY	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,		
Db	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,		
QY	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,		
Db	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,		
QY	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,		
Db	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,		
QY	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,		
Db	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,		
QY	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,		
Db	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,		
QY	Fahney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,		
Db	Fahney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,		
QY	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,		
Db	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,		
QY	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,		
Db	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,		
QY	Rodriguez A.C., Grimskala U., Schmutz J., Myers R.M., Butterfield Y.S.,		
Db	Rodriguez A.C., Grimskala U., Schmutz J., Myers R.M., Butterfield Y.S.,		
QY	Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,		
Db	Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,		
QY	Jones S.J., Marra M.A.		
Db	Jones S.J., Marra M.A.		
QY	"generation and initial analysis of more than 15,000 full-length human		
Db	"generation and initial analysis of more than 15,000 full-length human		
QY	and mouse cDNA sequences."		
Db	and mouse cDNA sequences."		
QY	Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903 (2002).		
Db	Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903 (2002).		
QY	SEQUENCE FROM N.A.		
Db	SEQUENCE FROM N.A.		
QY	TISSUE=Brain;		
Db	TISSUE=Brain;		
QY	Strausberg R.		
Db	Strausberg R.		
QY	Submitted (Oct-2002) to the EMBL/GenBank/DBJ databases.		
Db	Submitted (Oct-2002) to the EMBL/GenBank/DBJ databases.		
QY	EMBL; BC038588; AAH38588.1; --		
Db	EMBL; BC038588; AAH38588.1; --		
QY	HSSP; Q90240; 1H8L.		
Db	HSSP; Q90240; 1H8L.		
QY	MEROPS; M14.951; --		
Db	MEROPS; M14.951; --		
QY	GO: 0004182; F:carboxypeptidase A activity; IEA.		
Db	GO: 0004182; F:carboxypeptidase A activity; IEA.		
QY	GO: 0008270; F:zinc ion binding; IEA.		
Db	GO: 0008270; F:zinc ion binding; IEA.		
QY	GO: 0007155; P:cell adhesion; IEA.		

Db 476 KEALLTFMEQVHRGIGKGVVTDEQGIPIANATISVSGINHGKVTASGGDYWRILNPGYRV 535
QY 512 TASAEGYHSVTRNCRVTFEBGPPFCNFVLTTPKQRLRELLAAGAKVP-PDL----- 562
Db 536 TAHAEGYTPSSKTCNVDDYDIGATQCNFILARSNWKRIREIMAMNGNRPIPRIDPSRPMT 595
QY 563 -RRRLRLRGQ 572
Db 596 QOREMQRRRLQ 606

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